

GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run on: July 21, 2002, 14:58:48 ; Search time 12014.9 Seconds

(without alignments)
17965.795 Million cell updates/sec

Title: US-09-702-216-1

Perfect score: 10315
Sequence: 1 ttctctcggaaggtcctt.....gttatctcaaaaaaaaaa 10315

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Listing first 45 summaries

GenBank: *
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2: gb_hcg: *
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29: em_vl: *
30: em_hcg_hum: *
31: em_hcg_inv: *
32: em_hcg_other: *
33: em_hcg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	2486.4	24.1	2596	5	AF346838
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ALIGNMENTS

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DEFINITION Homo sapiens zinc finger transcription factor TRPS1 mRNA, complete cds.
ACCESSION AF183810
VERSION AF183810.1 GI:6684533
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 10011)
Momeni, P., Gloeckner, G., Schmidt, O., von Holtum, D., Albrecht, B.,
Gillesen-Kaesbach, G., Hennekam, R., Melnick, P., Zabel, B.,
Rosenthal, A., Horsthemke, B. and Ludecke, H.-J.
Mutations in a new gene, encoding a zinc-finger protein, cause
tricho-rhino-phalangeal syndrome type I

TITLE

JOURNAL Nat. Genet. 24 (1), 71-74 (2000)

MEDLINE 2 (bases 1 to 10011)

REFERENCE

AUTHORS

Gillesen-Kaesbach, G., Hennekam, R., Melnick, P., Zabel, B.,
Momeni, P., Gloeckner, G., Schmidt, O., von Holtum, D., Albrecht, B.,
Gillesen-Kaesbach, G., Hennekam, R., Melnick, P., Zabel, B.,
Rosenthal, A., Horsthemke, B. and Ludecke, H.-J.

TITLE Rosenthal, A., Horsthemke, B. and Lueddecke, H.-J.
Direct Submission
Submitted (06-Sep-1999) Institut fuer Humangenetik,
Universitaetsklinikum, Hufelandstr. 55, D-45122 Essen, Germany
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BASH COUNT 3067 a 1963 c 2056 g 2925 t
ORIGIN

Query Match 97.1%; Score 10011; DB 9; Length 10011;
Best local similarity 100.0%; Pred. No. 0;
Matches 10011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION PROGRESS *** 4 ordered pieces.
AC013815
AC013815.11 GI:18252021
VERSION HTG: HTGS_PHASE2; HTGS_FUJITOP; HTGS_ACTIVERLIN.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 165813)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Qy 6721 aaagaagaagaagaatcaggaactgaactgaactgaactgaactgaactgaactgaact 6780
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RESULT 3
AC023142/c 159505 bp DNA linear HTG 20-AUG-2000
LOCUS Homo sapiens chromosome 8 clone RP11-558b2, WORKING DRAFT SEQUENCE,
AC023142 19 unordered pieces.
ACCESSION AC023142.4 GI:9795980
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 159505)
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 159505)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Aug 11, 2000 this sequence version replaced g1:9558667.

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H_NH0558B02
----- Summary Statistics -----
Sequencing vector: M13; 100x
Sequencing vector: plasmid; 0x
Chemistry: Dye-Primer ET; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 152349 bases at least Q40
Consensus quality: 154057 bases at least Q30
Consensus quality: 154743 bases at least Q20
Insert size: 141000; agarose-fp
Insert coverage: 4.80 in Q20 bases; sum-of-coverage
Quality coverage: 4.85 in Q20 bases; sum-of-coverage
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1432: contig of 1432 bp in length
* 1433 1532: gap of unknown length

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FEATURES	Location/Qualifiers
source	1. .159505

[illegible]

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DEFINITION	Human sapiens zinc finger protein GC79 mRNA, complete cds.					
ACCESSION	AF264784					
VERSION	AF264784.1	GI:10644121				
KEYWORDS						
SOURCE	human					
ORGANISM	Homo sapiens					
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AUTHORS	Chang,G.T.G., Steenbeck,M., Schippers,E., Blok,L.J., van Weerden,M.M., van Aalwijk,D.C., Eussen,B.H., van Steenbrugge,G.J. and Brinkman,A.O.					
TITLE	Characterization of a Zinc-Finger Protein and Its Association With Apoptosis in Prostate Cancer Cells					
JOURNAL	J. Natl. Cancer Inst. 92 (17), 1414-1421 (2000)					
PUBMED	10974077					
REFERENCE	2 (bases 1 to 5507)					
AUTHORS	Chang,G.T.G.					
TITLE	Direct Submission					
JOURNAL	Submitted (09-MAY-2000) Endocrinology & Reproduction, Erasmus University Rotterdam, P.O. Box 1738, Rotterdam 3000 DR, Netherlands					
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BASE COUNT 1694 a 1213 c 1234 g 1366 t
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Query Match 51.3%, Score 5295; DB 9; Length 5507;
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 REFERENCES
 1 (sites)
 Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,
 Nishikawa, T., Nagai, K., Sugano, S., Takahashi, Fujii, A., Hara, H.,
 Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K.,
 Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J.,
 Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y., and Oshima, A.
 NEDO human cDNA sequencing project
 Unpublished (2000)
 2 (bases 1 to 2596)
 Isogai, T. and Otsuki, T.
 Direct Submission
 Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
 Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 (E-mail:genomics@htl.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
 NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan: cDNA full insert
 sequencing: Research Association for Biotechnology; cDNA library
 construction, 5'- & 3'-end one pass sequencing and clone selection:
 Helix Research Institute (supported by Japan Key Technology Center
 etc.) and Department of Virology, Institute of Medical Science,
 University of Tokyo.
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Qy	3787	gaatgaatctatccgatctbaaggaagaaggaagctctggagaagcgactatagaaa	3846
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RESULT 7			
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DEFINITION	Xenopus laevis atypical GATA protein TRPS1 (TRPS1)	linear	VR7 25-APR-2001
ACCESSION	AF346838	transcript, complete cds.	mRNA, zygotic
VERSION	AF346838.1	GI:13785804	
KEYWORDS			
SOURCE	African clawed frog.		
ORGANISM	Xenopus laevis		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;		
AUTHORS	Xenopodius; Xenopus.		
TITLE	1 (bases 1 to 4625)		
JOURNAL	Malik,T.H., Shoichet,S.A., Latham,P., Kroll,T.G., Peters,L.L. and Shivasani,R.A.		
PUBMED	Transcriptional repression and developmental functions of the atypical vertebrate GATA protein TRPS1		
ADDITIONAL	EMBO J. 20 (7), 1715-1725 (2001)		
ADDITIONAL	11285235		
ADDITIONAL	2 (bases 1 to 4625)		
ADDITIONAL	Malik,T.H. and Shivasani,R.A.		
ADDITIONAL	Submitted (08-FEB-2001) Adult Oncology, Dana Farber Cancer Institute, 44 Binney Street, SM 854, Boston, MA 02115, USA		
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BASE COUNT 1482 a 1025 c 976 g 1142 t
ORIGIN

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RESULT	8		
LOCUS	AKO21511	1587 bp	mRNA linear PRI 29-SEP-2000
DEFINITION	Homo sapiens cDNA FL111449 fis, clone HEMBA1001411.		
ACCESSION	AKO21511		
VERSION	AKO21511.1 GI:10432707		
SOURCE	oigo capping: fis (full insert sequence).		
KEYWORDS	Homo sapiens embryo; 10 weeks whole embryo; mainly head cDNA to mRNA, clone_id:HEMBA1 clone:HEMBA1001411.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (sites)		

Hosogai, T., Ito, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugeno, S., Shiratori, A., Sudo, H., Wadaetsuma, M., Hosokita, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Morikawa, K., Ono, Y., Takaguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawaji, S., Saito, K., Yamamoto, J., Wakatsuki, A., Nakamura, Y., Nagahara, K., Masuno, Y., Niimura, K., and Iwayanagi, T. (2010) Human cDNA sequencing project

Unpublished (2000)
2 (bases 1 to 1587)
Isogai, T. and Otsuki, T.
Direct Submission
Submitted (23-AUG-2000)

NEO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction, 5', 3' end and one pass sequencing and clone selection; Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.

Location/Qualifiers

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7288 tatgtcagctacttttagtaaatatttttggatagcgttgacaagatagatcttat 7347

301 TATGGCAGCTACCTTTTACGAGAAATTTTGGATACGGTTGACACGATGATCTTAT 360

361 TCCATACGCTCTTATTATTGCATTAATTTCATTTTTCGCTTCATTATATACATA 420

421 TTTCGCTGAGAGAAGGTTGGCCTTTTGAAGAGACAAAAATTATTATACACTTAA 480

Db 481 CACTCCITTTTGACATATTAAAGCCCTTATTCATCTCAAGATATATTATAAAATTT 540

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LOCUS Homo sapiens CDNA FLJ11408 fis, clone HEMBA1000822.
DEFINITION AK021470
ACCESSION AK021470
VERSION AK021470.1 GI:10432662
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens embryo, 10 weeks whole embryo, mainly head cDNA to mRNA, clone lib:HEMBA1 clone:HEMBA1000822.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
Magatsuna,M., Hosoliri,T., Kaku,Y., Kodaira,H., Kondo,H.,
Sugawara,M., Takehashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
Ono,Y., Takiguchi,S., Matanabe,S., Kimura,K., Murakami,K.,
Ishii,S., Kawai,T., Saito,K., Yamamoto,Y., Wakamatsu,A.,
Nakamura,Y., Nagahari,K., Masuhara,Y., Nimomiya,K. and Iwayanagi,T.
NEDO human cDNA sequencing project
Unpublished (2000)
2 (bases 1 to 1551)
Isogai,T. and Otsuki,T.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) to the DDBJ/EMBL/GenBank databases. Takao
REFERENCE Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana,
AUTHORS Kisarazu, Chiba 292-0812, Japan (E-mail: genomics@hri.co.jp,
Tel:81-438-52-3951, Fax:81-438-52-3952)
JOURNAL NEDO human cDNA sequencing project supported by Ministry of
TITLE International Trade and Industry of Japan; cDNA full insert
COMMENT Sequencing: Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center
etc.) and Department of Virology, Institute of Medical Science,
University of Tokyo.
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 VERSION AC103571
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 SOURCE Norway rat.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE
 AUTHORS
 1 (bases 1 to 165191)
 Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
 Alsbrooks,S.L., Amaralunge,H.C., Aye,J.R., Banks,T., Barbarris,J.,
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 Stone,H., Sutton,A., Svalek,A., Taber,P., Tamerisa,A., Tamerisa,K.,
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 Wellington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S.,
 Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
 Weinstock,G. and Gibbs,R.
 TITLE
 JOURNAL
 Unpublished
 2 (bases 1 to 165191)
 REFERENCE
 AUTHORS
 Worley,K.C.
 TITLE
 Direct Submission

JOURNAL

COMMENT

Submitted (29-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Dec 21, 2001 this sequence version replaced gi:17149303.

 Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu

 Project Information
 Center project name: CGKO
 Center clone name: CH230-23014

 Summary Statistics
 Assembly program: Phrap; version 0.990329First call to
 findPthApList

Consensus quality: 134429 bases at least Q40
 Consensus quality: 145218 bases at least Q20
 Consensus quality: 153975 bases at least Q20
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 Quality coverage: 0x in Q20 bases; agarose-1p estimation
 Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 70 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
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RESULT 11
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LOCUS Xenopus laevis atypical GATA protein TRPS1 (TRPS1) mRNA, maternal
DEFINITION Transcriptional repressor.
ACCESSION AF346837

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VERSION AF346837.1 GI:13785802
KEYWORDS African clawed frog.
SOURCE xenopus laevis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
REFERENCE Xenopodinae; Xenopus.
AUTHORS Malik,T.H., Sholchet,S.A., Iatham,P., Kroll,T.G., Peters,I.L. and
Shivasani,R.A.
TITLE Transcriptional repression and developmental functions of the
atypical vertebrate GATA protein TRPS1
JOURNAL EMBO J. 20 (7), 1715-1725 (2001)
PUBMED 11285235
AUTHORS Malik,T.H. and Shivdasani,R.A.
REFERENCE 2 (bases 1 to 3767)
AUTHORS Malik,T.H. and Shivdasani,R.A.
JOURNAL Direct Submission
SUBMITTED (08-FEB-2001) Adult Oncology, Dana Farber Cancer
Institute, 44 Binney Street, SM 854, Boston, MA 02115, USA
FEATURES
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 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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 JOURNAL Unpublished
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 Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
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 REFERENCE 1 (bases 1 to 310002)
 AUTHORS Momeni, P., Glockner, G., Schmidt, O., von Holtum, D., Albrecht, B.,
 Gillissen-Kaesbach, G., Hennekam, R., Melnecke, P., Zabel, B.,
 Rosenthal, A., Horsthemke, B. and Ludecke, H.J.
 TITLE Mutations in a new gene, encoding a zinc-finger protein, cause
 trichorhino-phalangeal syndrome type I
 JOURNAL Nat. Genet. 24 (1), 71-74 (2000)
 MEDLINE 20082812
 PUBMED 10615131
 REFERENCE 2 (bases 1 to 310002)
 AUTHORS Glockner, G., Rosenthal, A., Ludecke, H.-J. and Horsthemke, B.
 TITLE Direct Submission
 JOURNAL Submitted (16-AUG-1999) Genome Analysis, Institute of Molecular
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Dh 34878 GTCTTTTAGATGTTCAAAATCTCAGTAGCTTTGTTGTTGGGTTTAGATATTTGTC 34819
OY 5222 caacacgtacccattttaaanaaacaatgctcctgacgtcctcgtatgtatttcattta 5281
Dh 34818 CACACATGTAACCATTTTAAAAACAAATGCTCGATGCTTCTGTAGTATTTCAATTTTA 34759
OY 5282 gccaggtattcttctctgtgtgtgtgtgaacagatgagattgtcttcttaagcctcct 5341
Dh 34758 GCCAGGTATTTCTTTCTTGTGTGTGATGACAGATGAGATTTGCTTTCTTAACCTCTCT 34699
OY 5342 gttggttactaatctcaatttgacattataactaaagaaagatccctcaattcaaaagca 5401
Dh 34698 GTTGGTACTATATCTACCTTGGCACATTAATACATAAGAAATCCCTCAATTTCAAAACCA 34639
OY 5402 tagatgatacaaatgtcagacagctgtgttaattgttttagacacatgagattcttc 5461
Dh 34638 TAGATGATTAACAAATGTCAACCGTGGGTTTAATTTGTTAGAACATGSGAATTTCTTC 34579
OY 5462 acaaggtaacctgtgattattattatttcttctgtgttaataataattccaaacttg 5521
Dh 34578 ACAAGGTAACTGCTGTAATTTATTTATTTCTTTTGGTTAAATATTAATTTCCAAACTTTG 34519
OY 5522 tggtaagcagcgtctaaaggttaacgtttacacaaagacagacatgtgtatattaccaccc 5581
Dh 34518 TGGTACGACAGCTCTAAGGTTAGCTTACCAAGATGACAGATGAGTGTATGTACACACC 34459
OY 5582 aatcccttcataatgatacagattagttaaagtgcattaaataggattccttagag 5641
Dh 34458 AATCCCTTCAATTAATGTATACAGATTATAGTTAGTACATTAATAATAGGATTTCTAGAG 34399

OY 5642 tatgtccctacagaactttaaacttaactlaagccttgtaaaacatacgaaggagaag 5701
Dh 34398 TATGTCCCTATTAAGACTTTTAACTTAAGGCTTTGTAATAATATCCATGAGGGGAAG 34339
OY 5702 ctccctacagcctaacgtctcagggaaatagggctaaataactgaacataaataattgctt 5761
Dh 34338 CTCTCAGCAATTAAGCTCTAAGGAAATAGGCTTAATAATACAGCTTAATTAATTTGTT 34279
OY 5762 aaaggtgctgttagtcagacctcaatgtctgtcaagaagatgatatgtacaagagact 5821
Dh 34278 AAAGGTGCTGTTAGTGAGAGCTCAATGCTGTCACAAAGATGATGATACAAAGACTGCT 34219
OY 5822 ttaataatltgcattatattgtcccaacacagtagttatttctgccaagagagatgaga 5881
Dh 34218 TTAAATTAATTTGCATTAATATTTGTCACACAGATGATTTATTTTTCACAGGAGATGGA 34159
OY 5882 agatatacagactgactgactgactgactgactgactgactgactgactgactgactg 5941
Dh 34158 AGATTTTCAAGCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 34099
OY 5942 gacacaataggaanaaaaaaactatttctcagtaataataataatgatatcattcaaa 6001
Dh 34098 GAACAATAAGGAANAANAANAATTTTCTAGTAATATTAATGATTAATTAATTTCAAA 34039
OY 6002 taatgtgctgacataatgataatatttctcaaggtgaagatgacacaaagatat 6061
Dh 34038 TATGTTGCTGACATATTTGATTAATTAATTTTCTACAGTATGATGATGATGATGAT 33979
OY 6062 tccatcatgcatagtagtagtgcagctgcagctgcagctgttaccattgcaatgtgac 6121
Dh 33978 TCCATCATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 33919
OY 6122 aaacaaggtlaatgaagaactatttctatgagtagatatactcttctgtgtgtgtg 6181
Dh 33918 AAACAAGGATTAAGCAACTATTCTTATGAGATATACCTTTGATGATGATGATG 33859
OY 6182 tgcattaaagttgaacaggttaacatgaaacaaatgaagagttcgtatatagtatgag 6241
Dh 33858 TGCATTTAAAGTTGTAAACGGTTAATCAATGAACAAAGAAAGTTCTGTATTAATGATG 33799
OY 6242 aaacaagaagaatgaataatatttctagcctccttaggaanaaaggttagactta 6301
Dh 33798 AAAACAAGAGGAAATGAAATTTTGTGCTTCTTAGGAAAAAGGATGACATTA 33739
OY 6302 ttcaatlcaagtaactt 6361
Dh 33738 TTCAATCCAAAGACTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 33679
OY 6362 aagatgataacataatactcttcttattgtctgtgtatgattcaatagaacatttc 6421
Dh 33678 AAGATGATTAACATATATATCTTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 33619
OY 6422 agaaattattttagaaggtgtgtgaatcgcgaacgtatatttttttttttttttttt 6481
Dh 33618 AGAATATATTTTGAATAGTGTGCTGAAATCTGCAACGCTGATTTTATTTTATTTTAT 33559
OY 6482 agtcgacttgcactcacttttataatattcgaatgagagttgtatgtatgttctgt 6541
Dh 33558 AGTCGATTTGACTCCATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 33499
OY 6542 tgggttgttcttcttcaagagtcgcgggtcttgcttcttaagatgagagagatga 6601
Dh 33498 TGGGTGTTGTTCTTTTCAAGTGCAGGCTGCTGTTGTTTAAAGTTGATGATGACAGTA 33439
OY 6602 gagttacaaggttgcaggtgtgtgagagagatgaagtaaaaaatgcttctcgaat 6661
Dh 33438 GAGTTCAACAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 33379
OY 6662 tgtgttcaatttcaatttgcatttttctgttgcattataaaaaaagagaagaaga 6721
Dh 33378 TGTGTTGCTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 33319

QY 6722 aagcaagagacagaatacgaagtaagtcctcgtcctgaagttcattgttaagagcctt 6781
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Db 33318 AAGCAAGACACAAATTCAGGACTAGCTCCTCCTGCTTCATTTGTTAACGGGCTT 33259
QY 6782 altctgaatcaccctgctcgtagctcaahaltccacataaactgaaataaagaatgga 6841
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Db 33258 ATTCTGATCTCACCTGTCCCGTAGCTCAATATTCAACATTAACGTAATTAAGAAGTGGGA 33199
QY 6842 atgagagccttgacatccaattatgtgagtcaattatcctcctcctgaagatttgatg 6901
|||||
Db 33198 ATGAGGAGCTTTGACATTCMAATTAATGATGATTAATTTCTCTTGGAATTTTATG 33139
QY 6902 gatgcattccaataatgtatagccagacttgagagtgacaaatcaagaatcccaaaagag 6961
|||||
Db 33138 GATGCATCTCAAAATTTATAGCGACTTGAAGGAGATTAAGTCTTAATAAAGAGAG 33079
QY 6962 agagcattcccccaacaacatalttaatttctctagtaaaagaataaagaatgcat 7021
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Db 33078 AGGAGATWCCCCCAACAACATTAATTTCTAGTAAATAAAGAAATACAGAAATGCAT 33019
QY 7022 cgtggaatcctctaaagcaacatatactatgtagcagcttaaalcaagcaaaacagaa 7081
|||||
Db 33018 CGTGGCATCTTTAAGCAACATTAATCTATGATGAGCTTAAATCAGGAAACACAGAA 32959
QY 7082 gtttggttaacttggaacatagcaagtaacttcttgaggcaaaactactcaatagc 7141
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Db 32958 GTTGGTTAACTTGGGCAATATGACAAAGTATTACTTTTGGGCAAAACTACTCATTAAGC 32899
QY 7142 aatttctcagtggtcggaacaaataggttcttatttcttgacatgatgccttita 7201
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Db 32898 AATWTCWAGTGTGCGACACAAATAGTTCWTTATTTTGGCATGTATGCGCTTTTGA 32839
QY 7202 ttttcattcaatttttttttttctcagagaagacatagatagatcaactacatagaaa 7261
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Db 32838 TTTTCATTCATTTTTTTTTTTTCTCAGACACAGATAGATGATACCTACCATTTGAAA 32779
QY 7262 atacatacactatctctggaatatattatgtgcagtcacttctttagtaaaataatttg 7321
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Db 32778 ATACATATWCACTATCTTGAATATTATGATGAGTCACTACTTTTAGTAAATTTTGTG 32719
QY 7322 gataagcttgacaagcagatagacttattccactccttattattgataatttatttcc 7381
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Db 32718 GATAGCGTWGACACGATACATCTTAATTCATCTTATTAATTTGAATTTTATTTTC 32659
QY 7382 atttttgcttcatattatatacatatttgggtggaagaggttgaggcttttttgaag 7441
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Db 32658 ATTTTTCGTTTATATTATATACATATTGTTGGGAGAGAGAGTGGGCTTTTGTGAAG 32599
QY 7442 agacaaaatttatatacaactaaacactccttcttttgacatataaagccttattcc 7501
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Db 32598 AGACAAAATTTTATTAACACTTAACACTCCCTTTTGTGACATATTAAAGCCTTTATTC 32539
QY 7502 atcctcacaagatatataaaatttatttctttaaattgaagatttccgaatttattc 7561
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Db 32538 ATCTCTCAACATATATTATAAAATTTATTTTAAATTTTAAATTTTGAATTTTATTTAT 32479
QY 7562 ctlaaatitgatttaaacagactatattgtagaagaaacttttttaagaagaaattc 7621
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Db 32478 CTAAATTTGATTTTAAACAGCATATTATGATGAGAACTTTTAAATAGGAATTTTC 32419
QY 7622 atgagatttagaaatttctcctccttggaagagcctccctgtagatgaatgagtgc 7681
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Db 32418 ATGATGATWTTAGGAATTTTCTCTCTGGAAAAGGCTTCCCTGATGAAAATGATGTGC 32359
QY 7682 cagctaaatitggtgcatitaaacitgaataatatttlaaatatttgcataatcc 7741
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Db 32358 CAGCTAAATTTGTGTGCCATTTAAACCTGAAAAATATTTTAAATTTTATTTTATTTAT 32299
QY 7742 taaatitgaacttggatcaaacatttaagccaagagcagctcagctcctcattcctcc 7801
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Db 32298 TAAATTTAGCTTTGATCAAACTTTAGGCCAGGACAGCATGCTCATATTTCTTCTC 32239
QY 7802 ttctcaactcttctcctacatcaactcctctgatacattctcgttgttggaataga 7861
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Db 32238 TTTCTACCTCTTCTCTCACTACACTCACTCTGTATTTATTTGTTGTTGGATAGAAA 32179
QY 7862 altcataagagccaacccatcccaagaagttgttgatltggaagaacacatacactacc 7921
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Db 32178 ATCAATAAGAGCCACACCATCTCACAGCTTGTGATTTAGAGAGACACTACATGACTCC 32119
QY 7922 aagtatagagaaaagagcagagcctcaatgtataactcgttagtccaagaagaaagag 7981
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Db 32118 AAGTATATGAAAAGAGACAGAGCTCTAATGATTAACCTGTGTGTTCAAAAAGAAAAG 32059
QY 7982 tatggcaattcctctacatgacatagtagatttttttaactactttaagtagt 8041
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Db 32058 TATGCCAATTTCTCTCACTACACTCACTCTGTATTTTATTTTAACTTTTAAAGTATG 31999
QY 8042 gatgtctgtctcaactgtcgttctttagtgaagtagatttttataaacaagacatgg 8101
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Db 31998 GATGTTCTGTCTTAACCTGTCTGTTTAGTGAAGTAGATTTTATTAACAAACCATGC 31939
QY 8102 ggaattcttctgaagtaattaaatgaagaggaagaaagtaactcttaagagctcttg 8161
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Db 31938 GGATTTCTTTCTAAGGTAATTAATTAAGAGGAAAAGATCTTTTAAAGCTCTTGG 31879
QY 8162 ttgaagccttgtagcacatattgttataatgtgacatgtgcacataactattatga 8221
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Db 31878 TTGAAGCCTGTGTTAGCAATTTATTTATTTGACATGTCCACATATATCTATTTATGA 31819
QY 8222 tccaatgaaatacagctcccaaaaalataaalyalatalatlttaaaatgacctgaga 8281
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Db 31818 TTCAATGCAATTAACGCTCCAAAATTTAAATGATATATTTTAAATGCCGAGGA 31759
QY 8282 aatacatttttcttaataaactggaagagctcaglatggtatlaaataattatggcc 8341
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Db 31758 AATACATTTTCTTAAATAAAGTGAAGAGTCCAGTATGCTATTAATAATTTATGACC 31699
QY 8342 tccgtgtgtgtgcacaaacatcacaaagtgagccgttcttgaagccgtggaactctg 8401
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Db 31698 TCCGTGTGTGTGTGTGCAAAAACATCACAAATGACCGGTTTGAAGCCTGTGAACCTG 31639
QY 8402 cccgtttagtaataaaaaatlaalgalcttctagaggggaalatalctccacagtggt 8461
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Db 31638 CCCGTTTAGCAATTAATAATTAATCATTTCTAGAGGGGAATATCTGCATCCAGTGGT 31579
QY 8462 ggaagtgtggaatgaagaagcgtgtgtcctctgtgtgtatgacagccttctgct 8521
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Db 31578 GGAATGTGAGTAAGAAAGCTGTGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 31519
QY 8522 taagttagagagagtcacactttagctactgttcttgggttgagagccatgcaaaaaa 8581
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Db 31518 TAAAGTGAAGAGAGGTCACACTTACCTACCTCTTTGTTTGAAGCCATGGCAAAAAA 31459
QY 8582 aaaaaagaaaaaagatcaagtcgtcttggtagagccagtaagtgaaagcttgctgact 8641
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Db 31458 AAAAAAGAAAAAAGATCAAGTCGTCCTGTGTGAGCCAGTAAGGTTAAAGCTGTGCTG 31399
QY 8642 gtccaagggccaaggaatattggaagattgaatgaactgtgagatcacaactaataat 8701
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Db 31398 GTCCAGGCAACAGCAAAATTTGAGGAATTAAGTAAGCACTGATCAAACTAAATAT 31339
QY 8702 tctaatcaaggttaggtactgtttagtggaaattctacacagcaagcaactgcaaatgaa 8761
|||||
Db 31338 TCTAATCAAAAGCTAGACTGTTAGCTGGAATTTATACAGACAGCACTGCAAAATGAGAA 31279
QY 8762 gaagatgaagagagcccgctcggaacttggagggcattgttatttcccaaaaaagac 8821
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Db 31278 GAAGATGAGAGAGAGCCCGCTCGGACTTTGAGAGGCACTGTTATTTCCAAAGAAAGAC 31219
QY 8822 ggcgaagggagagagagatgattcttgcagagagacttcccttggtttccagtaactg 8881
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Db 31218 GGCAGAGGAGAGGAGATGATTTCTTGCAGAGCACTTCTTTGTGTTTCAAGTACTGT 31159
QY 8882 ttcatagacagttggctcactgttccctgtaggtgcagagttgcttagaagatccca 8941
|||||

[illegible]

	OY	10022	ggtatggtttatatgatcttaacttccattcacccttcaggaacaaataagaatcatlty	10081
Dn	30018	GGTATGCTTTATTAAAGTAATTCACCTTCACCTCCAGC-----CAATAGGAATAAATACGATCATPFG	29961	
OY	10082	taatatafatatatbatatcac-----ag	10106	
Dn	29960	TAAATACAG	29901	
OY	10107	gcctctcguaanbaaataggatgnaatcaaacaccattccaataanaattattacttaatl	10166	
Dn	29900	GCGTCGTCTGAATTGAAATGGTAGAACCAATCACCATTTCAAANAATATTACTTATAT	29841	
OY	10167	gataaagccttgantcctctaactgittgttgttgcgttttttttccttaaccaacaalc	10226	
Dn	29840	GATTAAGAAGCTGCAGCTCTCTCAACTGGTGGTGGCTTTGATTTTTTTTCTTAAAACAACACTC	29781	
OY	10227	tcttactagttagatttgytgbtaaasagatataciactagtlcttclogsaagaattaacaal	10286	
Dn	29780	TTCCACTGATATATATTTTGTGTAAAAAGATATATATCTCTTCTTCAGAGAGAT---	AACA 29724	
OY	10287	aaaatctggttatlttcaaanaa 10311		
Dn	29723	TAAAAATGGTTTATTTCAAAAACA 29699		
RESULT 14				
AC103571/c		165191 bp	DNA	linear HTG 21-DEC-2001
LOCUS		Rattus norvegicus clone CH230-2301d,	*** SEQUENCING IN PROGRESS	
DEFINITION		*** 70 unordered pieces.		
ACCESION		AC103571		
VERSION		AC103571.2 GI:17975672		
KEYWORDS		HTG; HMGs-PHASE1.		
SOURCE		Norway rat.		
ORGANISM		Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
REFERENCE		1 (bases 1 to 165191)		
AUTHORS		Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alspbrooks,S.L., Amaraturung,H.C., Are,J.R., Banks,T., Barbafala,J., Benton,J.J., Blumage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowls,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burich,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carrier,W., Cavaazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederlich,D.A., Delaney,K.R., DeLado,O., Dean,A.I., Ding,Y., Dinw.H.H., Douthwaite,K.J., Draper,H., Duhan-Hochs,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Hollaway,C., Holins,B., Homsi,F., Howard,S., Huber,J., Hulys,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivert,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Koryah,J., Kovar,C., Kitlovic,J., Kureshi,A., Landry,N., Deal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,M., Louiseged,H., Lozador,R.U., Lu,X., Lucier,A., Lucifer,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mayhewley,E., Meledod,M.P., Mesdor,M., Mei,G., Metzger,M., Miner,G., Minner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,M., Neal,D., Newtonson,J., Newton,N., Nguyen,N., Nguyen,N., Nickerson,E., Nwokkenko,S., Oguh,M., Okwuonu,G., Oraguynye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Prims,E., Pul,L., Quiles,M., Ren,Y., Rives,M., Rojes,A., Rojnookan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabori,P., Tamerisa,A., Tamerisa,K.		

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Tang, H., Tansey, J., Taylor, C., Taylor, P., Telford, B., Thomas, N.,
Thomas, S., Usmani, K., Vasquez, U., Vera, V., Villalón, D., Yinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Wattinson, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S.,
Worley, K., Wu, C., Wu, Y., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

Direct Submission
Unpublished
2 (bases 1 to 165191)
Morley, K.C.

Direct Submission
Submitted (29-NOV-2001)

Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced gi:17149303.

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GSKO

Center clone name: CH230-23014

Summary Statistics

Assembly program: Phrap; version 0.990329first call to

findhaplist

Consensus quality: 134429 bases at least Q40

Consensus quality: 145218 bases at least Q30

Consensus quality: 153975 bases at least Q20

Estimated insert size: 139772; sum-of-contigs estimation

Quality coverage: 0x in Q20 bases; agarose-fp estimation

Quality coverage: 2x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 6105: contig of 6105 bp in length
* 6106 6205: gap of unknown length
* 11261 11261: contig of 5056 bp in length
* 11362 17360: contig of 5999 bp in length
* 17361 17460: gap of unknown length
* 17461 23466: contig of 6006 bp in length
* 23467 23566: gap of unknown length
* 23567 27210: contig of 3644 bp in length
* 27211 32384: contig of 5074 bp in length
* 32385 32484: gap of unknown length
* 32485 38098: contig of 5614 bp in length
* 38099 38198: gap of unknown length
* 38199 42291: contig of 4093 bp in length
* 42292 42391: gap of unknown length
* 42392 46438: contig of 4047 bp in length
* 46439 46538: gap of unknown length
* 46539 49455: contig of 2917 bp in length
* 49456 49555: gap of unknown length
* 49556 53903: contig of 4248 bp in length
* 53904 56759: contig of 2856 bp in length
* 56760 56859: gap of unknown length
* 56860 59279: contig of 2420 bp in length
* 59280 59379: gap of unknown length
* 59380 62454: contig of 3075 bp in length
* 62455 62554: gap of unknown length
* 62555 64184: contig of 1630 bp in length
* 64185 64284: gap of unknown length

64285 66279: contig of 1995 bp in length
* 66280 66379: gap of unknown length
* 66380 69681: contig of 3302 bp in length
* 69682 69781: gap of unknown length
* 69782 72311: contig of 2530 bp in length
* 72312 72411: gap of unknown length
* 72412 74528: contig of 2117 bp in length
* 74529 74628: gap of unknown length
* 74629 77130: contig of 2502 bp in length
* 77131 77230: gap of unknown length
* 77231 80302: contig of 3072 bp in length
* 80303 80402: gap of unknown length
* 80403 83283: contig of 2881 bp in length
* 83284 83383: gap of unknown length
* 83384 85292: contig of 1909 bp in length
* 85293 85392: gap of unknown length
* 85393 87794: contig of 2402 bp in length
* 87795 87894: gap of unknown length
* 87895 90673: contig of 2779 bp in length
* 90674 90773: gap of unknown length
* 90774 93297: contig of 2524 bp in length
* 93298 93397: gap of unknown length
* 93398 95571: contig of 2174 bp in length
* 95572 95672: gap of unknown length
* 95673 98066: contig of 2393 bp in length
* 98067 98166: gap of unknown length
* 98167 101300: contig of 2864 bp in length
* 101301 101330: gap of unknown length
* 101331 103263: contig of 2133 bp in length
* 103264 103363: gap of unknown length
* 103364 104700: contig of 1337 bp in length
* 104701 104800: gap of unknown length
* 104801 106936: contig of 2136 bp in length
* 106937 107036: gap of unknown length
* 107037 109153: contig of 2117 bp in length
* 109154 109253: gap of unknown length
* 109254 110533: contig of 1280 bp in length
* 110534 110633: gap of unknown length
* 110634 111959: contig of 1326 bp in length
* 111960 112059: gap of unknown length
* 112060 113766: contig of 1607 bp in length
* 113767 114908: contig of 1142 bp in length
* 114909 115008: gap of unknown length
* 115009 116433: contig of 1425 bp in length
* 116434 116533: gap of unknown length
* 116534 119159: contig of 2626 bp in length
* 119160 119259: gap of unknown length
* 119260 120589: contig of 1330 bp in length
* 120590 120689: gap of unknown length
* 120690 122551: contig of 1862 bp in length
* 122552 122651: gap of unknown length
* 122652 123809: contig of 1158 bp in length
* 123810 123909: gap of unknown length
* 123910 125359: contig of 1450 bp in length
* 125360 125459: gap of unknown length
* 125460 126567: contig of 1108 bp in length
* 126568 126667: gap of unknown length
* 126668 128366: contig of 1699 bp in length
* 128367 128466: gap of unknown length
* 128467 129734: contig of 1268 bp in length
* 129735 129834: gap of unknown length
* 129835 130997: contig of 1163 bp in length
* 130998 131097: gap of unknown length
* 131098 132474: contig of 1377 bp in length
* 132475 132574: gap of unknown length
* 132575 133816: contig of 1242 bp in length
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[illegible]

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LOCUS AX067304
DEFINITION Sequence 8 from Patent WO0078960.
ACCESSION AX067304
VERSION AX067304.1 GI:12544928
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 996)
AUTHORS Yagin,J. and Mitchem,J.L.
TITLE Compositions and methods for the therapy and diagnosis of breast
cancer.
JOURNAL Patent: WO 0078960-A 8 28-DEC-2000;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers
source 1..996
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BASE COUNT 299 a 148 c 188 g 361 t
ORIGIN

Query Match 9.1%; Score 943.4; DB 6; Length 996;
Best Local Similarity 99.7%; Pred.No.1.2e-178;
Matches 966; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db 988 TTGACAGTC 996

Search completed: July 21, 2002, 22:24:41
Job time: 26753 sec

PR 16-NOV-1999; 99US-0440676.
PR 16-NOV-1999; 99US-0440677.
PR 29-NOV-1999; 99US-0450810.
PR 02-DEC-1999; 99US-0453137.
PR 08-MAR-2000; 2000US-0453137.
XX
PA (E0SB-) EOS BIOTECHNOLOGY INC.

XX Mack D, Gish KC;
XX WPI: 2000-638216/61.
XX P-PSDB: AAB00190.

PT Screening drug candidates for their ability to modulate breast cancer
PT by contacting the drug to a cell expressing an expression profile gene
PT and determining modulation of expression of the gene

PS Disclosure: Fig 46A-D; 258pp; English.

CC New methods for screening drug candidates are described which
CC comprise adding a drug candidate to a cell that expresses a protein
CC selected from BCL1, BCL2, BCL7, BCLN1, BCLN5, BCLN2, BCLN3, BCLN4
CC and BCLN5 or their fragments and determining the effect of the drug
CC on the expression of those proteins. Antibodies to breast cancer
CC genes (specifically BCL1 or its fragment (BCL1p1 or BCL1p2)) are
CC useful for inhibiting and treating breast cancer in individuals who
CC are non-responsive to anti-estrogen and positive for estrogen
CC receptor. Compositions comprising BCL1 or a nucleic acid encoding
CC BCL1 are useful for eliciting an immune response in an individual.
CC The antibodies are also useful for the diagnosis and prognosis of
CC breast cancer and for screening compositions which modulate the
CC breast cancer phenotype. The method allows rapid and simple
CC detection of lymph node metastases.

XX Sequence 10320 BP; 3174 A; 2005 C; 2096 G; 3042 T; 3 other;

Query Match 99.6%; Score 10278.2; DB 21; Length 10320;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 10309; Conservative 1; Mismatches 4; Indels 7; Gaps 2;

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Db 10320 a 10320

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AAC74759; AC

AC AAC74759;

DT 08-FEB-2001 (first entry)

Human ORFX ORF314 polynucleotide sequence SEQ ID NO:627.

KM Human: open reading frame; ORF3; detection; cytotoxic; hepatotropic;
 KM Vulerary; antipapillary; antipapillomelan; neoplastic; neuroprotective;
 KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;
 KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KM antiviral; antibacterial; antifungal; antineoplastic; antithyroid;
 KM antitumoric; gene therapy; cancer; proliferative disorder; hypertension;
 KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KM cardiovascular disease; diabetes mellitus; hydrolydism; SCID; AIDS;
 KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KM thrombosis; contraceptive; ss.

OS Homo sapiens.

PN WO20000584 / 3-A2.
XX

FD-001-2000.
XX

31-MAR-2000; 2000MO-US08621.

PR	02-APR-1999:	99US-0127636
PR	31-MAR-1999:	99US-0127607

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

PI Shimkets RA, Leach M;

DR WPI; 2000-602362/57.

Novel nucleic acids are

PT neurodegenerative di

PS Claim 5; Page 743-75

CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43

sequences have activities such as: cyto

CC osteopage;c:anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antididiabetic; hypotensive; dermatologic; immunosuppressive;
CC antitumormetory; antibacterial; antiviral; antitungal; antirheumatic;
CC antihypoid; and antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORX-associated disorder. The
CC nucleic acids can be used to express ORX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,

CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage
CC nocturnal haemoglobinuria, anti-inflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
SQ Sequence 10319 BP; 3176 A; 2006 C; 2093 G; 3043 T; 1 other;

SQ Sequence 10319 BP; 3176 A; 2006 C; 2093 G; 3043 T; 1 other;

Query Match	99.4%;	Score 10255;	DB 21;	Length 10319;
Best Local Similarity	99.8%;	Pred. No. 0;		
Matches 10300;	Conservative	0;	Mismatches 12;	Indels 9;
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QY	61	gcgagacataaggttcttcgaacaagcgataaattctcgtataaagcccgatcttaata	120
Dp	62	gcgagacataaggttcttcgaacaagcgataaattctcgtataaagcccgatcttaata	121
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Qy	8402	ccctgttttagtaataaattatgattcttcaagagggaataatctgcctcaagtgt	8461

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ID	ABAL4483	Standard; DNA; 10004 BP.	
AC			
XX	ABAL4483;		
XX			
DJ	23-JAN-2002	(first entry)	
XX			
DE		Human nervous system related polynucleotide SEQ ID NO 6814.	
XX			
KW	Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;		
KW	immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;		
KW	antiparkinsonian; antischizoid; antiandemic; antiarthritis; cancer;		
KW	antihemetic; hepatotropic; cerebroprotective; antiinflammatory;		
KW	antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;		

PR 05-JAN-2001: 2001US-0259678.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 P1 Rosen CA, Barash SC, Ruben SW;
 XX WPI: 2001-541565/60.
 DR
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system
 PT cancers and metastases -
 PS
 XX Disclosure: SEQ ID NO 6814; 1701bp + Sequence Listing; English.
 CC
 CC The invention relates to novel genes (ABAI1004-AB21534) and proteins
 CC (AB14678-AB18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemia;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 10004 BP; 3292 A; 1809 C; 1695 G; 3208 T; 0 other;
 Query Match 63.9%; Score 6587.2; DB 22; Length 10004;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 6657; Conservative 0; Mismatches 13; Indels 12; Gaps 5;

DB 6199 AAGTACAGTACCCACTTTTGGACTCCCTTGGATCAATGATCTCCAGAGTGAAC 6140
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PD	
EE	17-JAN-2001; 2001WO-US01334
XX	31-JAN-2000; 2000US-0179065
PR	04-FEB-2000; 2000US-0180528
PR	24-FEB-2000; 2000US-0184564
PR	02-MAR-2000; 2000US-0186350
PR	16-MAR-2000; 2000US-01989674
PR	17-MAR-2000; 2000US-01900756
PR	18-APR-2000; 2000US-0198123
PR	19-MAY-2000; 2000US-0205515
PR	07-JUN-2000; 2000US-0209667
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PR	11-JUL-2000; 2000US-0216880
PR	11-JUL-2000; 2000US-0217487
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PR	14-JUL-2000; 2000US-0218290
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PR	14-AUG-2000; 2000US-0224518
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PR	14-AUG-2000; 2000US-0225213
PR	14-AUG-2000; 2000US-0225214
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PR	14-AUG-2000; 2000US-0225268
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PR	18-AUG-2000; 2000US-0225759
PR	22-AUG-2000; 2000US-02266219
PR	22-AUG-2000; 2000US-0226686
PR	23-AUG-2000; 2000US-0227182
PR	30-AUG-2000; 2000US-0227009
PR	01-SEP-2000; 2000US-0228624
PR	01-SEP-2000; 2000US-0229287
PR	01-SEP-2000; 2000US-0229343
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PR	05-SEP-2000; 2000US-0229345
PR	05-SEP-2000; 2000US-0229509
PR	06-SEP-2000; 2000US-0229513
PR	06-SEP-2000; 2000US-0230437
PR	08-SEP-2000; 2000US-0231242
PR	08-SEP-2000; 2000US-0231243
PR	08-SEP-2000; 2000US-0231414
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PR	12-SEP-2000; 2000US-0232081
PR	14-SEP-2000; 2000US-0231966
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PR	14-SEP-2000; 2000US-0233398
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PR	14-SEP-2000; 2000US-0233400
PR	14-SEP-2000; 2000US-0234201
PR	14-SEP-2000; 2000US-0233063
PR	14-SEP-2000; 2000US-0233064
PR	21-SEP-2000; 2000US-0234223
PR	21-SEP-2000; 2000US-0234224
PR	25-SEP-2000; 2000US-0234274
PR	25-SEP-2000; 2000US-0234997
PR	26-SEP-2000; 2000US-0234998
PR	27-SEP-2000; 2000US-0235498
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PR	27-SEP-2000; 2000US-0235885
PR	29-SEP-2000; 2000US-0236327
PR	29-SEP-2000; 2000US-0236327

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system
PT cancers and metastases -
xx
PS Disclosure; SEQ ID NO 6815; 1701bp + Sequence Listing; English.
XX

The invention relates to novel genes (ABA11004-ABA21534) and proteins (AB1678-AB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemia; and CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPRO at ftp.wipro.int/pub/published_pat_sequences.

Sequence 5825 BP; 1856 A; 1120 C; 1006 G; 1843 T; 0 other;

SQ

Query Match Best Local Similarity 56.2%; Score 5793; DB 22; Length 5825; Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2.

QY 3422 gactccagcgctttaacaatcaatcaataaaacacggtgcagattataggagag 3481
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Db	5045	ACCAAAATGTAAAAATGAAGGTCCTTGATGTAGTAAAAACAGAAATTCATTAGAG	4966
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QY	4322	gattgaagctttgcataatgattgcaatggtagcaagttgcaacttccaaigtgaagatg	4381
Db	4925	GATGATGCTTTGCATATAGATGTGCATGCTGTACAGTGGACCTTCCAGTGGAGATAG	4866
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Db	4805	GAAACAATGCCAAATGGAAAAAATGGAAAACCTTAAGTAAAACCTTAGACATCTTACCA	4746
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Db	4565	GAAGAATGGAAAGATGTTAAACAAATCACTTTTAAACCGTTAATGATCAAAACATCTTG	4506
QY	4742	gctaataitactgtgggaataatccatagaagatatccagagatgaataataatatt	4801
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QY	5222	caacatgttacccaattttaaanaaagatgctccgtatgctttgtgaaggttcaattta	5281
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QY	5582	aatcccttcaataatgtatacagattttagtaagatagatcaataatagattctttagaag	5641
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QY	5702	ctctctcagcaactagctcagaagaaatagggcttcaatactaacgaacatitaaatattgct	5761
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Db	3485	AAAGTGCTGTATAGTCGAGCCTCAATGCTGCTTCAACAGATGATGTACAAAGACTGACT	3426
QY	5822	ttaataattgcatatatttcccaacacagatgtttttttggccaagggatgtgata	5881
Db	3425	TTAATAATTGGCATTAATTTCTCCCAACACAGTAGTTTATTTTGTGCCACGGAGATGAGA	3366
QY	5882	agatattcaagctctcagatgacgtcagatlaacttattcattlaaagaagttggga	5941
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QY	5942	gaacaaataggaaaaaaaactatatttttcagtaaatcttaatgtatatacttcaaa	6001
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QY	2827	gtcalgcacatccacataccaagaagagacccaatltgacatccaggtctctacatctgc	2886
Db	817	gtcalgcacatccacataccaagaagagacccaatltgacatccaggtctctacatctgc	876
QY	2887	taactccagaactcctaanaatlyggagagccagttctcgaagtgctgtgtgaagagagaagac	2946
Db	877	taactccagaactcctaanaatlyggagagccagttctcgaagtgctgtgtgaagagagaagac	936
QY	2947	tggaaagagaaagagagcggtctaaagaagaaagtttggaccgagagttccagtgtaaccttc	3006
Db	937	tggaaagagaaagagagcggtctaaagaagaaagtttggaccgagagttccagtgtaaccttc	996
QY	3007	gcaatgtgacatlyggagagagagacatctctcgggggagttccgtaataccaagaacaa	3066
Db	997	gcaatgtgacatlyggagagagagacatctctcgggggagttccgtaataccaagaacaa	1056
QY	3067	gctctgggggctctgcagccgcgtgtctctgcaccaagagcagagacaaagactctaaaggata	3126
Db	1057	gctctgggggctctgcagccgcgtgtctctgcaccaagagcagagacaaagactctaaaggata	1116
QY	3127	gtcccaaatlyggagagcccgccacatctgcgcgcgcactcttaatgagctgtgggtlygaaacca	3186
Db	1117	gtcccaaatlyggagagcccgccacatctgcgcgcgcactcttaatgagctgtgggtlygaaacca	1176
QY	3187	aggagatccctgcaggggcgcgcgcgcgtctgcgcgaagagagttctggggccctcccccagagat	3246
Db	1177	aggagatccctgcaggggcgcgcgcgcgtctgcgcgaagagagttctggggccctcccccagagat	1236
QY	3247	atctcgcacatcgagagaaacaagaatcccaagagatgataatccagtcctcgtgtgaagagcgata	3306
Db	1237	atctcgcacatcgagagaaacaagaatcccaagagatgataatccagtcctcgtgtgaagagcgata	1296
QY	3307	gaaggtcccggtgttttttggccaattgcctgcaccacaagaactctctctgcgcgaaga	3366
Db	1297	gaaggtcccggtgttttttggccaattgcctgcaccacaagaactctctctgcgcgaaga	1356
QY	3367	atgcacaatlygcgcgaataatgatacgaacgcgtgtggccctctacacaagaagttctactgcaccc	3426
Db	1357	atgcacaatlygcgcgaataatgatacgaacgcgtgtggccctctacacaagaagttctactgcaccc	1416

QY	3427	caaagcctttaaatcatcattaaacaaacaaacggttgagagattatlttagagagagaca	3486
Db	1417	caaagcctttaaatcatcattaaacaaacaaacggttgagagattatlttagagagagaca	1476
QY	3487	gaaagcgcttaaccccaagagagacttcggttgagagcttcaacaaacagcagagggca	3546
Db	1477	gaaagcgcttaaccccaagagagacttcggttgagagcttcaacaaacagcagagggca	1536
QY	3547	gcaatlgagagcaagatlgaaatggaaagcccggtlttagagagagggcagaaagatcattacg	3606
Db	1537	gcaatlgagagcaagatlgaaatggaaagcccggtlttagagagagggcagaaagatcattacg	1596
QY	3607	aaagtcacccagagagaaatttcacactcccaagcctaagtgaaatacagaagccagagttac	3666
Db	1597	aaagtcacccagagagaaatttcacactcccaagcctaagtgaaatacagaagccagagttac	1656
QY	3667	tgaactaaagacacttcgtctgcagccagtcctgtgtcagccaactctgatatccaa	3726
Db	1657	tgaactaaagacacttcgtctgcagccagtcctgtgtgtcagccaactctgatatccaa	1716
QY	3727	aaaagatgcaacacttgcacattcagataaagaatctcctaagaagaatgcaggagatccag	3786
Db	1717	aaaagatgcaacacttgcacattcagataaagaatctcctaagaagaatgcaggagatccag	1776
QY	3787	gaaatagttatccgtatcttgtaagggaaaggaattctctgagagagcgatccataagaa	3846
Db	1777	gaaatagttatccgtatcttgtaagggaaaggaattctctgagagagcgatccataagaa	1836
QY	3847	aatacagagacactgtggaacaccccaattattcacccacagcgacccatttgaaagtl	3906
Db	1837	agtaacagagacactgtggaacaccccaattattcacccacagcgacccatttgaaagtl	1896
QY	3907	accagtaaccacttlttgacttcccttltgatatagatccagatccagatgagcttgtt	3966
Db	1897	accagtaaccacttlttgacttcccttltgatatagatccagatccagatgagcttgtt	1956
QY	3967	ggctcgcggtctcgagtaataataagctctccggttccctggaaatccgacacttgatgc	4026
Db	1957	ggctcgcggtctcgagtaataataagctctccggttccctggaaatccgacacttgatgc	2016
QY	4027	acggtgcctggccttaacaaatcccttgccaacatactgacctalccacacttcaattcgc	4086
Db	2017	acggtgcctggccttaacaaatcccttgccaacatactgacctalccacacttcaattcgc	2076
QY	4087	ctctcaatttticagcgttggatcagacaatgacatccctctagatlttggagatcaagc	4146
Db	2077	ctctcaatttticagcgttggatcagacaatgacatccctctagatlttggagatcaagc	2136
QY	4147	attccagacactggcccaactcgcgaacacggtgtcccaagagagaaacgaaagcaccacaa	4206
Db	2137	attccagacactggcccaactcgcgaacacggtgtcccaagagagaaacgaaagcaccacaa	2196
QY	4207	atgtaaaaaatgaaggtccctctgaatgtgtgtataaaacagagaagtgtgataagatctc	4266
Db	2197	atgtaaaaaatgaaggtccctctgaatgtgtgtataaaacagagaagtgtgataagatctc	2256
QY	4267	agaatgaacttccaacaaatgt	4326
Db	2257	agaatgaacttccaacaaatgt	2316
QY	4327	atgcttgcataatgagttgcacatgtgtacagtgtgaccttccagatgcaagatgacagc	4386
Db	2317	atgcttgcataatgagttgcacatgtgtacagtgtgaccttccagatgcaagatgacagc	2376
QY	4387	atcttggccggaacaaatagatcttaaacacatccagaggggctgtcataggaaca	4446
Db	2377	atcttggccggaacaaatagatcttaaacacatccagaggggctgtcataggaaca	2436
QY	4447	atgcaacaagtgtg-aaaaaaatgaaaacctaaagaatgaaaaccttaagacttaagacaat	4505
Db	2437	atgcaacaagtgtgaaaaaaatgaaaaccttaagaaatgaaaaccttaagacttaagacaat	2496
QY	4506	taatatagaataagtttcttctgtatgtggaatccaatagctgtgttaatglttataagagact	4565

Db 2497 taatagaataggtttcttctgacggaattcaatagctgttaagtcttaagaacct 2556
QY 4566 attaaaaaatactcaatagagccttgcttatacaacatg 4605
Db 2557 attaaaaaatactcaatagagccttgcttatacaacatg 2596

RESULT 8
AAD06845
ID AAD06845 standard: DNA; 2327 BP.

AC AAD06845;

DT 06-AUG-2001 (first entry)

DE Human breast cancer specific gene-3 (BCSG-3) #1.

KM Human: breast cancer specific gene-3; BCSG-3; cytostatic; vaccine;
KW breast cancer; therapeutic; gene therapy; ds.

OS Homo sapiens.

PN W020013779-A2.

PD 31-MAY-2001.

PF 22-NOV-2000; 2000MO-US32056.

PR 23-NOV-1999; 99US-016973.

PA (DIAD-) DIADEXUS INC.

PI Salceda S, Cafferkey R, Reclon H, Sun Y;

DR WPI; 2001-367602/38.

PT Novel breast cancer specific gene for diagnosing, monitoring, staging,
imaging, preventing and treating cancers, particularly breast cancer -
PS Claim 1; Page 50; 66pp; English.

CC The invention relates human breast cancer specific genes (BCSG's) and
their corresponding proteins. BCSG is useful for diagnosing, staging,
monitoring, imaging, preventing and treating breast cancers. BCSG is also
useful for inducing an immune response against a target cell expressing
mutations in BCSG, thereby determining if a human with the genetic lesion
is at risk for breast cancer or has breast cancer. BCSG antibodies
labelled with paramagnetic ions or radioisotopes is useful for imaging
breast cancers; while BCSG antibodies conjugated to a cytotoxic agent is
useful for treating breast cancer. BCSG is useful in the rational design
of new therapeutics for imaging and treating cancers. BCSG is also used
in gene therapy. The present DNA sequence is human breast cancer specific
gene-3 (BCSG-3) or Gene ID 274731.

Sequence 2327 BP; 720 A; 371 C; 443 G; 765 T; 28 other;

Query Match 21.9%; Score 2257.6; DB 22; Length 2327;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2293; Conservative 0; Mismatches 32; Indels 3; Gaps 3;

QY 6898 gatgatgatcctcaaatgtatagccagacttgagaggtgacaattaaagatcctaaaa 6957
Db 1 gatgatgatcctcaaatgtatagccagacttgagaggtgacaattaaagatcctaaaa 60
QY 6958 agagagagagattcccccaaacacacatattattttcttgtaaaagaataacgaat 7017
Db 61 agagagagagattcccccaaacacacatattattttcttgtaaaagaataacgaat 120
QY 7018 gcatcgtggcaatccttaagcaaatattatctgtgagctgcttaaaacgcaaacacc 7077

Db 121 gcatcgtggcaatccttaagcaaatattatctgtgactgtcttaacacgcaaacacc 180
QY 7078 agaagttgttacttggtgcaatatagaagattacttttgggcaaaactcact 7137
Db 181 agaagttgttacttggtgcaatatagaagattacttttgggcaaaactcact 240
QY 7138 aagcaattctctagtgtgtcgacacaaataggtcttatttttggcatgtacct 7197
Db 241 aagcaattctctagtgtgtcgacacaaataggtcttatttttggcatgtacct 300
QY 7198 ttatttttactcaatttttttttctcagacagacatagtagtaacgactgacctg 7257
Db 301 ttatttttactcaatttttttttctcagacagacatagtagtaacgactgacctg 360
QY 7258 gaaatcacatcactatctcttggaattataggtcagctcacttttggtaaatatt 7317
Db 361 gaaatcacatcactatctcttggaattataggtcagctcacttttggtaaatatt 420
QY 7318 ttggatagcgttgacagatagatcttaccactcttattttatgtatattat 7377
Db 421 ttggatagcgttgacagatagatcttaccactcttattttatgtatattat 480
QY 7378 ttcatattttgcttcaattatatacaaatlttggtgagaagagttlggcttttg 7437
Db 481 ttcatattttgcttcaattatatacaaatlttggtgagaagagttlggcttttg 540
QY 7438 aaagagacaaaatttatatacaactaaacactccttttggcatataaagcctta 7497
Db 541 aaagagacaaaatttatatacaactaaacactccttttggcatataaagcctta 600
QY 7498 ttccatctctcagatatattataaattattttttaaattgaattctgaattct 7557
Db 601 ttccatctctcagatatattataaattattttttaaattgaattctgaattct 660
QY 7558 ttatcttaattgtgatttttaaacagactatagtgaacggaacttttttaaggaa 7617
Db 661 ttatcttaattgtgatttttaaacagactatagtgaacggaacttttttaaggaa 720
QY 7618 ttcatgtatgttaggaattttctcttggaagaagctctccctgtgagaaatgat 7677
Db 721 ttcatgtatgttaggaattttctcttggaagaagctctccctgtgagaaatgat 780
QY 7678 gtgcagactaaactgtgtgcatttaaaactgaaataatttaaatattgtcat 7737
Db 781 gtgcagactaaactgtgtgcatttaaaactgaaataatttaaatattgtcat 840
QY 7738 attcaatttgagtttgatcaaaactttaggcaggaacagctacgttctcatct 7797
Db 841 attcaatttgagtttgatcaaaactttaggcaggaacagctacgttctcatct 900
QY 7798 tccctttctacitcttctcctacatcactcactcctgtattctgtgttgagatg 7857
Db 901 tccctttctacitcttctcctacatcactcactcctgtattctgtgttgagatg 960
QY 7858 aaaatcatataagcccaaccatctcagaacgtgtgtgattgagagacatcatga 7917
Db 961 aaaatcatataagcccaaccatctcagaacgtgtgtgattgagagacatcatga 1020
QY 7918 ctccaagtatatagaaaagacagagctcctaatltgataactctgttagtcaaaaggaa 7977
Db 1021 ctccaagtatatagaaaagacagagctcctaatltgataactctgttagtcaaaaggaa 1080
QY 7978 agagatgccaattctctcctacatgacatattgagatttttttaacacttttaga 8037
Db 1081 agagatgccaattctctcctacatgacatattgagatttttttaacacttttaga 1140
QY 8038 tagtgatgttctgttcttaactgtctgtttagtgaagtagatctttataaacaagc 8097
Db 1141 tagtgatgttctgttcttaactgtctgtttagtgaagtagatctttataaacaagc 1200
QY 8098 atggagatcttcttcaaggtatataatgaaaggaagaaagatattccttaacagctc 8157
Db 1201 atggagatcttcttcaaggtatataatgaaaggaagaaagatattccttaacagctc 1260

	RESULT	9	AAH16992	standard; cDNA; 1587 BP.
ID	AAH16992	standard; cDNA; 1587 BP.		
AC	AAH16992;			
XX				
DT	26-JUN-2001	(first entry)		
XX				
DE	Human cDNA sequence SEQ ID NO:16281.			
XX				
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss			
OS	Homo sapiens.			
XX				
PN	EPI074617.A2.			
PD				
XX	07-FEB-2001.			
PF	28-JUL-2000; 2000EP-0116126.			
XX				
PR	29-JUL-1999; 99JP-0248036.			
XX	27-AUG-1999; 99JP-0300253.			
PR	11-MAY-2000; 2000JP-0118776.			
XX	02-MAY-2000; 2000JP-0183767.			
PR	09-JUN-2000; 2000JP-0241899.			
XX				
PA	(HELI-) HELIX RES INST.			
P1	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;			
P1	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;			
DR	WPI: 2001-318749/34.			
XX				
PT	Primer sets for synthesizing polynucleotides, particularly the 5602			
PT	full-length cDNAs defined in the specification, and for the detection			
PT	and/or diagnosis of the abnormality of the proteins encoded by the			
PT	full-length cDNAs -			
XX				
PS				
XX				
PP	Claim 8; SEQ ID 16281; 2537pp + CD ROM; English.			
CC	The present invention describes primer sets for synthesizing 5602			
CC	full-length cDNAs defined in the specification. Where a primer set			
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary			
CC	to the complementary strand of a polynucleotide which comprises one of			
CC	the 5602 nucleotide sequences defined in the specification, where the			
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination			
CC	of an oligonucleotide comprising a sequence complementary to the			
CC	complementary strand of a polynucleotide which comprises a 5'-end			
CC	sequence and an oligonucleotide comprising a sequence complementary to a			
CC	polynucleotide which comprises a 3'-end sequence, where the			
CC	oligonucleotide comprises at least 15 nucleotides and the combination of			
CC	the 5'-end sequence/3'-end sequence is selected from those defined in			
CC	the specification. The primer sets can be used in antisense therapy and			
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,			
CC	particularly full-length cDNAs. The primers are also useful for the			
CC	detection and/or diagnosis of the abnormality of the proteins encoded by			
CC	the full-length cDNAs. The primers allow obtaining of the full-length			
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and			
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to			
CC	AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632			
CC	represent oligonucleotides, all of which are used in the exemplification			
CC	of the present invention.			
XX				
SQ	Sequence 1587 BP; 486 A; 244 C; 276 G; 581 T; 0 other:			
	Query Match	15.3%; Score 1580.6; DB 22; Length 1587;		
	Best Local Similarity	99.7%; Pzed. No. 0;		
	Matches 1583; Conservative	0; Mismatches	4; Indels	0; Gaps
yy	taatttcttgataaaagaataacaagatcaccgcgtgggaatcgctttacgacccaattatc 7047			

Db 1 taatttcttagtaaaaaagaataacagaatgcgtggtgcaatcccttaagcaaatatc 60
 Qy 7048 tatgtgactgtttaaatacgaacaaacacagaagtgttgtaacttgggcaatagaca 7107
 Db 61 tagtggactgtttaaatacgaacaaacacagaagtgttgtaacttgggcaatagaca 120
 Qy 7108 agtataacttttgggcaaacactaacatgaagaatttctctagtggtgcggaacaa 7167
 Db 121 agtataacttttgggcaaacactaacatgaagaatttctctagtggtgcggaacaa 180
 Qy 7168 taagtcttcttaatttggcatgtagccttttattcttcaatatttttttttttc 7227
 Db 181 taagtcttcttaatttggcatgtagccttttattcttcaatatttttttttttc 240
 Qy 7228 agcagacatagtgtatcaactacagcatggaaaatacatatcactatcttggaaat 7287
 Db 241 agcagacatagtgtatcaactacagcatggaaaatacatatcactatcttggaaat 300
 Qy 7288 tatgtgcagcttacttctttagtaaaatatttggatagcgttgacaagatagactat 7347
 Db 301 tatgtgcagcttacttctttagtaaaatatttggatagcgttgacaagatagactat 360
 Qy 7348 tccataactcttctttagtaaaatatttggatagcgttgacaagatagactat 7407
 Db 361 tccataactcttctttagtaaaatatttggatagcgttgacaagatagactat 420
 Qy 7408 ttgttgagagaaggtgtggttttttggagaagacaaatcattataacactaa 7467
 Db 421 ttgttgagagaaggtgtggttttttggagaagacaaatcattataacactaa 480
 Qy 7468 caatccttctttagcaatataagccttattcactcctcaagatatttataaatt 7527
 Db 481 caatccttctttagcaatataagccttattcactcctcaagatatttataaatt 540
 Qy 7528 attttttaaattagaattctgaaatttttaacttaattgtaatttaagcagcta 7587
 Db 541 attttttaaattagaattctgaaatttttaacttaattgtaatttaagcagcta 600
 Qy 7588 ttatgtgaaggaacttttttaaggaattcagatgatttgaagaatttctcctc 7647
 Db 601 ttatgtgaaggaacttttttaaggaattcagatgatttgaagaatttctcctc 660
 Qy 7648 ggaataaggtctccctgtatgaataatgtagcagccttaaatgttgccatttaa 7707
 Db 661 ggaataaggtctccctgtatgaataatgtagcagccttaaatgttgccatttaa 720
 Qy 7708 actgaaataattttaaataattgtctatattcctaattgagcttggacaactta 7767
 Db 721 actgaaataattttaaataattgtctatattcctaattgagcttggacaactta 780
 Qy 7768 ggcagagacagctatgcttctcacttcttctcactcttctcactcactca 7827
 Db 781 ggcagagacagctatgcttctcacttcttctcactcttctcactcactca 840
 Qy 7828 cctctgtatcatctgttgttggatagaataacataaagagcacaacccatccaga 7887
 Db 841 cctctgtatcatctgttgttggatagaataacataaagagcacaacccatccaga 900
 Qy 7888 acgttgtgattgagagagacactacatgctcccaagatataagaaagagacagctc 7947
 Db 901 acgttgtgattgagagagacactacatgctcccaagatataagaaagagacagctc 960
 Qy 7948 taattgataactctgattgcaaaaaggaagagatgcccaattctctctacatgacat 8007
 Db 961 taattgataactctgattgcaaaaaggaagagatgcccaattctctctacatgacat 1020
 Qy 8008 attgagattttttaaacaactttaagaatgtagtctgtcttaacactgtctgt 8067
 Db 1021 attgagattttttaaacaactttaagaatgtagtctgtcttaacactgtctgt 1080
 Qy 8068 ttatgtgaagtagatttttataaacaagacatgggagattcttcttaagtagataat 8127
 Db 1081 ttatgtgaagtagatttttataaacaagacatgggagattcttcttaagtagataat 1140

Qy 8128 gagagaggaaaaaagatattcattcaacagctcttgttgaagcctgtgtagacattatgt 8187
 Db 1141 gagagaggaaaaaagatattcattcaacagctcttgttgaagcctgtgtagacattatgt 1200
 Qy 8188 ttataattgcacatgtgacataatcttattatgataatgcaatgcaatgcaatgcaat 8247
 Db 1201 ttataattgcacatgtgacataatcttattatgataatgcaatgcaatgcaatgcaat 1260
 Qy 8248 attaatgataatattttaaattgacatgaggaataatatttcttaataacaggaag 8307
 Db 1261 attaatgataatattttaaattgacatgaggaataatatttcttaataacaggaag 1320
 Qy 8308 agctcagatagcctattataaataattatagcctctgtgtgtgtgtgtgtgtgtgtgt 8367
 Db 1321 agctcagatagcctattataaataattatagcctctgtgtgtgtgtgtgtgtgtgtgt 1380
 Qy 8368 caaagtgacaggtcttggagacgtgtgacgtgctgctgctgtttagtaataaataatg 8427
 Db 1381 caaagtgacaggtcttggagacgtgtgacgtgctgctgctgtttagtaataaataatg 1440
 Qy 8428 attctagaaggagataatctgcacatcagtggtggaatgtggaatggaatggaatgga 8487
 Db 1441 attctagaaggagataatctgcacatcagtggtggaatgtggaatggaatggaatgga 1500
 Qy 8488 gtctgtctctgt 8547
 Db 1501 gtctgtctctgt 1560
 Qy 8548 tactgtctctgt 8574
 Db 1561 tactgtctctgt 1587

RESULT 10
 AAH15234
 ID AAH15234 standard; cDNA; 1551 BP.
 AC AAH15234;
 DE 26-JUN-2001 (first entry)
 XX Human cDNA sequence SEQ ID NO:13348.
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 PN EP1074617-A2.
 PD 07-FEB-2001.
 XX 28-JUL-2000; 2000BP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.

Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602
 full-length cDNAs defined in the specification, and for the detection
 and/or diagnosis of the abnormality of the proteins encoded by the
 full-length cDNAs -
 Claim 8; SEQ ID 13348; 2537bp + CD ROM; English.

XX The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13678 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX
 SQ Sequence 1551 BP; 476 A; 238 C; 285 G; 552 T; 0 other:

Query Match 14.9%; Score 1537; DB 22; Length 1551;
 Best Local Similarity 99.9%; Pred. No. 8.2e-315;
 Matches 1549; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 5306 gatgaacagatgagattgcttcttaagcctcctgttggttaacttaacttgaca 5365
 Db 1 gatgaacagatgagattgcttcttaagcctcctgttggttaacttaacttgaca 60
 QY 5366 cattataactaaagagatccctcaattcaaaagacataatgatacaaatgaagccg 5425
 Db 61 cattataactaaagagatccctcaattcaaaagacataatgatacaaatgaagccg 120
 QY 5426 tgggttaattgttagaacacatgagcattctctcaaggttaacgtcgtattatt 5485
 Db 121 tgggttaattgttagaacacatgagcattctctcaaggttaacgtcgtattatt 180
 QY 5486 tatttctctgtttaaataaataattccaaacttggtcagcagcgcttaagttac 5545
 Db 181 tatttctctgtttaaataaataattccaaacttggtcagcagcgcttaagttac 240
 QY 5546 gtacacacagactgacagttgtatgtacacgcaatcccttaataatgatacag 5605
 Db 241 gtacacacagactgacagttgtatgtacacgcaatcccttaataatgatacag 300
 QY 5606 atttaagtaagtagaataatagattcttagaagtagtctcctcaataactttaa 5665
 Db 301 atttaagtaagtagaataatagattcttagaagtagtctcctcaataactttaa 360
 QY 5666 cttaaggtttgttaaaactatccatgaaggaagcctcctcagcataactcgtcggga 5725
 Db 361 cttaaggtttgttaaaactatccatgaaggaagcctcctcagcataactcgtcggga 420
 QY 5726 aatagggcctaataactgaacattaataatgtttaagggcgcttagtgagagctca 5785
 Db 421 aatagggcctaataactgaacattaataatgtttaagggcgcttagtgagagctca 480
 QY 5786 atgctgtctacaagagatgatagtacaagagctgacttaataattgcatatattgtcc 5845
 Db 481 atgctgtctacaagagatgatagtacaagagctgacttaataattgcatatattgtcc 540
 QY 5846 caacacagtagttattttttgccaagagatgtagaagatattacaagcctactgatacga 5905
 Db 541 caacacagtagttattttttgccaagagatgtagaagatattacaagcctactgatacga 600
 QY 5906 ctgacagataactatttcaataagaagttggagagacaataaggaaaaaanaact 5965
 Db 5906 ctgacagataactatttcaataagaagttggagagacaataaggaaaaaanaact 5965

Db 601 ctgacagataactatttcaataagaagttggagagacaataaggaaaaaanaact 660
 QY 5966 attttctagaataataatattatgtataacttccaataatggtgctgacatattgaata 6025
 Db 661 attttctagaataataatattatgtataacttccaataatggtgctgacatattgaata 720
 QY 6026 attatttctacagtagcagtagatgcaacagataatccatcatcatgcatlaagagctc 6085
 Db 721 attatttctacagtagcagtagatgcaacagataatccatcatcatgcatlaagagctc 780
 QY 6086 tggctctgactagctgtttacatttgcacatgtaacaaagagtaagttaagcaacttt 6145
 Db 781 tggctctgactagctgtttacatttgcacatgtaacaaagagtaagttaagcaacttt 840
 QY 6146 ttatttgcagtagatcactccttttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6205
 Db 841 ttatttgcagtagatcactccttttgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
 QY 6206 atgaacaagaatgaagttctgtctataatgataaggaacaaagagaagaagaataat 6265
 Db 901 atgaacaagaatgaagttctgtctataatgataaggaacaaagagaagaagaataat 960
 QY 6266 ttatttgcacttaggaanaaagagtagacactatttccattccacttttttttttt 6325
 Db 961 ttatttgcacttaggaanaaagagtagacactatttccattccacttttttttttt 1020
 QY 6326 ttaatttttaagccttaactcaactgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 6385
 Db 1021 ttaatttttaagccttaactcaactgtatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1080
 QY 6386 ttatttgcctgttctatggtttatattgtaaacatttccaaacttttttttttttttt 6445
 Db 1081 ttatttgcctgttctatggtttatattgtaaacatttccaaacttttttttttttttt 1140
 QY 6446 tgggaactcgaacgctga--ttttttttgcatctgtatgcatatttgcattcatttt 6503
 Db 1141 tgggaactcgaacgctgaagtttttttttttttttttttttttttttttttttttttt 1200
 QY 6504 tacattatctgcagttgt 6563
 Db 1201 tacattatctgcagttgt 1260
 QY 6564 gtgcgggctctgctttcttaaaagtgtgagtagagaggttccaaacggttcgagctg 6623
 Db 1261 gtgcgggctctgctttcttaaaagtgtgagtagagaggttccaaacggttcgagctg 1320
 QY 6624 ttgtagcgaatgaagtttaaaaaaatgtcttctgtatgtgtgtgtgtgtgtgtgtgtgt 6683
 Db 1321 ttgtagcgaatgaagtttaaaaaaatgtcttctgtatgtgtgtgtgtgtgtgtgtgtgt 1380
 QY 6684 cattttttttgtgcattataaaaaaagagaagaagaagaagaagaagaagaagaaga 6743
 Db 1381 cattttttttgtgcattataaaaaaagagaagaagaagaagaagaagaagaagaagaaga 1440
 QY 6744 ctgaagtcctgtctgaagttcatgtttaacgagcctatttgcattcaccctgtcgt 6803
 Db 1441 ctgaagtcctgtctgaagttcatgtttaacgagcctatttgcattcaccctgtcgt 1500
 QY 6804 agctctaatattcacataactgaataaagaagttggaatgagagctgtg 6854
 Db 1501 agctctaatattcacataactgaataaagaagttggaatgagagagctgtg 1551

RESULT 11
 AAC79479
 ID AAC79479 standard; CDNA; 1009 BP.
 XX AAC79479;
 AC AAC79479;
 XX
 XX 07-FEB-2001 (first entry)
 XX
 XX cDNA sequence for human breast tumour clone #19606.
 XX

KW Human: breast tumour antigen: cytostatic; immunotherapy;
 KW breast cancer; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200061756-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 10-APR-2000; 2000MO-US09688.
 XX
 PR 09-APR-1999; 99US-0288950.
 PR 02-JUL-1999; 99US-0346327.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Reed SC, Xu J, Dillon DC;
 XX
 DR WPI: 2000-638568/61.
 XX
 PT A novel isolated polypeptide comprising an immunogenic portion of a
 PT breast cancer protein useful in the detection and treatment of breast
 PT cancer -
 XX
 PS
 XX
 CC Claim 4; Page 95; 95pp; English.
 CC
 CC The present sequence was isolated from a breast tumour cDNA library. It
 CC is provided in a specification relating to compounds for immunotherapy
 CC and diagnosis of breast cancer. Breast tumour antigens and the
 CC polynucleotides that encode them may be used in the production of a
 CC pharmaceutical composition to be used in the treatment of breast cancer.
 CC Proliferated T cells and incubated antigen presenting cells are also
 CC required. The polypeptides and polynucleotides may also be used to
 CC produce a vaccine.
 XX
 XX
 SQ Sequence 1009 BP; 316 A; 163 C; 193 G; 336 T; 1 other;

Query Match 9 8%; Score 1007; DB 21; Length 1009;
 Best Local Similarity 99.8%; Pred. No. 7.5e-203;
 Matches 1007; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7581 cgaagctatctgtacggaactcttttaatgaggaattcatgagtttaggaattt 7640
 DB 1 cgaagctatctgtacggaactcttttaatgaggaattcatgagtttaggaattt 7640
 QY 7641 ctctctggaaaaggctccctgtagatgaatgagtgccagctaaattgtgtcca 7700
 DB 61 ctctctggaaaaggctccctgtagatgaatgagtgccagctaaattgtgtcca 7700
 QY 7701 tttaaaactggaatatttttaattttgtcttatcttaattgagctttgata 7760
 DB 121 tttaaaactggaatatttttaattttgtcttatcttaattgagctttgata 7760
 QY 7761 aactttaggcagagccagctcagctctctctctctctctctctctctctca 7820
 DB 181 aactttaggcagagccagctcagctctctctctctctctctctctctctca 7820
 QY 7821 tcactaactctgtattatctctgtgtttggatagaaaataaagagccaacca 7880
 DB 241 tcactaactctgtattatctctgtgtttggatagaaaataaagagccaacca 7880
 QY 7881 tctcagaagctgtgagttgagagagacactacgactccaagtatatagaaaagac 7940
 DB 301 tctcagaagctgtgagttgagagagacactacgactccaagtatatagaaaagac 7940
 QY 7941 agagctcaattgatactcgtatgtaaaagaaaagagatagcccaattctctac 8000
 DB 361 agagctcaattgatactcgtatgtaaaagaaaagagatagcccaattctctac 8000
 QY 8001 atgacatattgagatttttttaatacaactttaagatagtgatgtctgttcaacty 8060
 DB 421 atgacatattgagatttttttaatacaactttaagatagtgatgtctgttcaacty 8060

QY 8061 ttctgttttaagtgaagctagatttttaataaacaagcatgaggatcttcttaagtaa 8120
 DB 481 ttctgttttaagtgaagctagatttttaataaacaagcatgaggatcttcttaagtaa 8120
 QY 8121 tattaatgagaaggaataaatactttaaagctcttctgaagctgtgtagaac 8180
 DB 541 tattaatgagaaggaataaatactttaaagctcttctgaagctgtgtagaac 8180
 QY 8181 attatgttataatgacatgacacatacttatgctccaatgacaatgacac 8240
 DB 601 attatgttataatgacacatgacacatacttatgctccaatgacaatgacac 8240
 QY 8241 caaaaatattaagtgatataattttaaalyccctggagaaatatacttttctlaata 8300
 DB 661 caaaaatattaagtgatataattttaaalyccctggagaaatatacttttctlaata 8300
 QY 8301 actgaagagctcagatgagctatataaataatttagctcctgtgtgtgtgcaa 8360
 DB 721 actgaagagctcagatgagctatataaataatttagctcctgtgtgtgtgcaa 8360
 QY 8361 aacatcaaaagtgcacccgcttgagacctgtggaactgtccctgttttagtaataaa 8420
 DB 781 aacatcaaaagtgcacccgcttgagacctgtggaactgtccctgttttagtaataaa 8420
 QY 8421 ttaatgacttctgaaggggaatctgcatccagtggtggaatgtagtaagaa 8480
 DB 841 ttaatgacttctgaaggggaatctgcatccagtggtggaatgtagtaagaa 8480
 QY 8481 gctgtgtgtcgtctgt 8540
 DB 901 gctgtgtgtcgtctgt 8540
 QY 8541 cttagctactgtcttctgt 8600
 DB 961 cttagctactgtcttctgt 8600

RESULT 12
 AA44852 standard; cDNA; 996 BP.
 ID AA44852;
 AC AA44852;
 XX
 XX
 DT 28-MAR-2001 (first entry)
 DE Human breast cancer related protein coding sequence SMQ ID NO: 8.
 XX
 KW Human: breast cancer; diagnosis; therapy; vaccine; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200078960-A2.
 XX
 PD 28-DEC-2000.
 XX
 PF 23-JUN-2000; 2000MO-US17536.
 XX
 PR 23-JUN-1999; 99US-0140903.
 PR 12-OCT-1999; 99US-0158980.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Yugiu J, Mitcham JL;
 XX
 DR WPI: 2001-041426/05.
 XX
 PT New polynucleotides encoding breast tumor specific proteins, useful for
 PT prevention, treatment and diagnosis of breast cancer -
 XX
 PS Claim 5; Page 120; 165pp; English.
 CC The present invention provides the coding sequences for a number of

CC breast cancer related proteins. These can be used in vaccinations
CC against, diagnosis of and treatment of cancer, particularly breast
CC cancer.
XX
SQ Sequence 996 BP; 299 A; 148 C; 188 G; 361 T; 0 other;

Query Match 9.1%; Score 943.4; DB 22; Length 996;
Best Local Similarity 99.7%; Pred. No. 2e-189;
Matches 966; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 5893 gctactggaatgactgacagatgaattatcttcaataagaattggagaacaatag 5952
DB 29 gctactggaatgactgacagatgaattatcttcaataagaattggagaacaatag 88
QY 5953 aaaaaaaactatcttctagtaataataatgattacattcaataatgagcct 6012
DB 89 aaaaaaaactatcttctagtaataataatgattacattcaataatgagcct 148
QY 6013 gacatattgaataattatcttcaatgagtgatgacaaagaattcattcattca 6072
DB 149 gacatattgaataattatcttcaatgagtgatgacaaagaattcattcattca 208
QY 6073 ttagagtcagttctgctgctgctgctgctgctgctgctgctgctgctgctg 6132
DB 209 ttagagtcagttctgctgctgctgctgctgctgctgctgctgctgctgctg 268
QY 6133 tgaagcaactatcttcaatgacatgacatgacatgacatgacatgacatgac 6192
DB 269 tgaagcaactatcttcaatgacatgacatgacatgacatgacatgacatgac 328
QY 6193 tgaatacgtgaatacgtgaatacgtgaatacgtgaatacgtgaatacgtga 6252
DB 329 tgaatacgtgaatacgtgaatacgtgaatacgtgaatacgtgaatacgtga 388
QY 6253 gaaatgaaatattttatgactactgagaaagggtagcactattcattcgaag 6312
DB 389 gaaatgaaatattttatgactactgagaaagggtagcactattcattcgaag 448
QY 6313 tacltt 6372
DB 449 tacltt 507
QY 6373 cataatccctcttttattgctctgctgctgctgctgctgctgctgctgctgct 6432
DB 508 cataatccctcttttattgctctgctgctgctgctgctgctgctgctgctgct 567
QY 6433 tgaatacgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 6491
DB 568 tgaatacgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 627
QY 6492 gcaatccatttttaataatgacatgacatgacatgacatgacatgacatgac 6551
DB 628 gcaatccatttttaataatgacatgacatgacatgacatgacatgacatgac 687
QY 6552 tctcttttcaagtgccggtctctctcttcaatgctgagtcagtcagtcagtc 6611
DB 688 tctcttttcaagtgccggtctctctcttcaatgctgagtcagtcagtcagtc 747
QY 6612 agttcgtgactgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 6671
DB 748 agttcgtgactgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 807
QY 6672 ttttcaattttgcatctttttgttgcattttaaanaaagaagaagaagaaga 6731
DB 808 ttttcaattttgcatctttttgttgcattttaaanaaagaagaagaagaagaaga 867
QY 6732 cagaatcaggaataagtcctctgctcagtttcaatgctgtaacgagtccttctg 6791
DB 868 cagaatcaggaataagtcctctgctcagtttcaatgctgtaacgagtccttctg 927
QY 6792 caactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 6851

DB 928 caactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 987
QY 6852 ttgacattc 6860
DB 988 ttgacattc 996

RESULT 13
AA82511
ID AA82511 standard; cDNA; 766 BP.
XX
AC AA82511;
XX
DF 18-JUN-2001 (first entry)
XX
DE Human breast tumour protein CDNA 15962.
XX
KW Human; breast cancer; tumour; cytosolic; gene therapy; ss.
XX
OS Homo sapiens.
PN W0200127276-A2.
PD 19-APR-2001.
PF 11-OCT-2000; 2000WO-US28255.
PR 12-OCT-1999; 99US-0417031.
PA (CORI-) CORIXA CORP.
PI Harlocker SL, Dillon DC, Xu J;
XX WPI: 2001-273773/28.
XX
PT New polypeptides encoded by polynucleotide sequences over-expressed in
PT breast tumor tissue are useful to detect, monitor and treat breast
PT cancer -
XX
PS Claim 1; Page 52; 52pp; English.
XX
CC The present sequence encodes a breast tumour-associated protein. It was
CC shown to have at least two-fold overexpression in breast tumour tissue.
CC The invention relates to an isolated polypeptide comprising at least an
CC immunogenic portion of a breast tumor-specific protein, or its
CC variant that retains the ability to react with antigen-specific antisera.
CC The breast tumour polynucleotides, polypeptides and antibodies are
CC useful for inhibiting development of breast cancer. The polynucleotides
CC may be used to design primers and probes for detecting and monitoring
CC breast cancer.
XX
SQ Sequence 766 BP; 250 A; 122 C; 137 G; 254 T; 3 other;

Query Match 7.4%; Score 761.4; DB 22; Length 766;
Best Local Similarity 99.5%; Pred. No. 5.1e-151;
Matches 762; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9243 ttcccaacatagaactgacagatatacttttcttctgctcagtcagtcagtc 9302
DB 1 ttcccaacatagaactgacagatatacttttcttctgctcagtcagtcagtcagtc 60
QY 9303 tgaataattgaataatataatgataatataatataatataatataatataatgata 9362
DB 61 tgaataattgaataatataatgataatataatataatataatataatataatgata 120
QY 9363 actggtttgtaagacacttgagtcctggttgaagagccatagagagtgcaagtat 9422
DB 121 actggtttgtaagacacttgagtcctggttgaagagccatagagagtgcaagtat 180
QY 9423 tattaatggcagaagggtttttaaatgctgcttcccaaggcagaagggttggg 9482
DB 181 tattaatggcagaagggtttttaaatgctgcttcccaaggcagaagggttggg 240

QY 9483 gtcaattttcttaagacagcgtgtaataatacactaggcagccaatagttgactatg 9542
 Db 241 gtcaattttnttaagacagcgtgtaataatacactaggcagccaatagttgactatg 300
 QY 9543 aagatgcaaaactattactagggcgtgataaaaatcagtttcttaagctacccaataag 9602
 Db 301 aagatgcaaaactattactagggcgtgataaaaatcagtttcttaagctacccaataag 360
 QY 9603 caaatgcaataataaacgccaatctccttagggcgagactattgacccaacttga 9662
 Db 361 caaatgcaataataaacgccaatctccttagggcgagactattgacccaacttga 420
 QY 9663 aaactttgggggagcagtcagggggggaacatccaatgccaatgtaaatatta 9722
 Db 421 aaactttgggggagcagtcagggggggaacatccaatgccaatgtaaatatta 480
 QY 9723 caagcaatttccagcagagaagaatgcttctcataaggaatgattcagttgtaagaa 9782
 Db 481 caagcaatttccagcagagaagaatgcttctcataaggaatgattcagttgtaagaa 540
 QY 9783 aagaaatcaattttagtctcgtatggaatactagaaatggtggtgataatgattctgtc 9842
 Db 541 aagaaatcaattttagtctcgtatggaatactagaaatggtggtgataatgattctgtc 600
 QY 9843 ttacaacacagaaatttttgcgttttatttatttatttgcgtttcagtagtgcatt 9902
 Db 601 ttacaacacagaaatttttgcgttttatttatttatttgcgtttcagtagtgcatt 660
 QY 9903 ctactcacaacaatgcttctggtgatttcttataagcaaaatcttccagcagcaaat 9962
 Db 661 ctactcacaacaatgcttctggtgatttcttataagcaaaatcttccagcagcaaat 720
 QY 9963 gctcgtttacatcttaacttgaataataagtttaccacagttac 10008
 Db 721 gctcgtttacatcttaacttgaataataagtttaccacagttac 766

RESULT 14
 ID AAH03367 standard; cDNA: 691 bp.
 AC AAH03367;
 XX
 DT 26-JUN-2001 (first entry)
 DE Human cDNA clone (5'-primer) SEQ ID NO:202.
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 OS Homo sapiens.
 XX
 PN EPI074617-A2.
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000FP-0116126.
 XX
 PR 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX
 PA (HELI-) HELIX RES INST.
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI: 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection

PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 PS Claim 1: SEQ ID 202; 2537pp + CD ROM; English.

CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03366 to AAH13628 and
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 691 BP; 211 A; 93 C; 104 G; 280 T; 3 other:

QY Query Match 6.6%; Score 681.6; DB 22; Length 691;
 Db Best Local Similarity 99.0%; Pred. No. 3.5e-134;
 Matches 684; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6988 taatttcttagtaaaaagataacagatgcatacgtgacatcccttaagcaacattc 7047
 Db 1 taatttcttagtaaaaagataacagatgcatacgtgacatcccttaagcaacattc 60
 QY 7048 tatgtgagctgcttaataatcagcaaacacccaagaattgttgaactgttgcaatgtgaca 7107
 Db 61 tatgtgagctgcttaataatcagcaaacacccaagaattgttgaactgttgcaatgtgaca 120
 QY 7108 agtattacttttgggcaaaactactcaatgaagaattctcagtgctcgacacaaa 7167
 Db 121 agtattacttttgggcaaaactactcaatgaagaattctcagtgctcgacacaaa 180
 QY 7168 taggttcttatttttggcagtcagtcctttttatttcaatcaattttttttctc 7227
 Db 181 taggttcttatttttggcagtcagtcctttttatttcaatcaattttttttctc 240
 QY 7228 agacagacatagtagtatacactagcattggaataacatcacatcattcttggaatt 7287
 Db 241 agacagacatagtagtatacactagcattggaataacatcacatcattcttggaatt 300
 QY 7288 tatgtgagctgcttaataatcagcaaacacccaagaattgttgaactgttgcaatgtgaca 7347
 Db 301 tatgtgagctgcttaataatcagcaaacacccaagaattgttgaactgttgcaatgtgaca 360
 QY 7348 tccactactcttattatgataatttatttcaatttttgccttcaattatataca 7407
 Db 361 tccactactcttattatgataatttatttcaatttttgccttcaattatataca 420
 QY 7408 ttgtgtgaggaagagtggtctttttggaagagcaaaaatttatatacaacaaa 7467
 Db 421 ttgtgtgaggaagagtggtctttttggaagagcaaaaatttatatacaacaaa 480
 QY 7468 caccctttttgacatataaagccttattccatctcgaagatatataataatt 7527
 Db 481 caccctttttgacatataaagccttattccatctcgaagatatataataatt 540
 QY 7528 atttttaataaagattcgaattatttttcttaattgtgatttaacagagcta 7587

Search completed: July 21, 2002, 21:50:11
Job time: 21033 sec

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OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 15:11:53 ; Search time 168.22 seconds

(without alignments)
15061.881 Million cell updates/sec

Title: US-09-702-216-1

Perfected score: 10315

Sequence: 1 ttccctccgcaagcgtcctt.....gtttattcaaaaaaaaaa 10315

Scoring table:

IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata2/ina/PCRTUS.COMB.seq:*
6: /cgn2_6/ptodata2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315.4	3.1	333	US-09-284-782-36	Sequence 36, Appl
2	72.4	0.7	19124	US-08-487-826B-13	Sequence 13, Appl
3	69.2	0.7	7218	US-08-232-463-14	Sequence 14, Appl
4	65	0.6	1456	US-09-037-135-1	Sequence 1, Appl
5	59.6	0.6	837	US-08-998-416-288	Sequence 288, App
6	59.4	0.6	2110	US-09-419-459-1	Sequence 1, Appl
7	58.8	0.6	636	US-08-998-416-1137	Sequence 1137, Ap
8	58.2	0.6	6243	US-09-056-075-1	Sequence 1, Appl
9	57.4	0.6	1004	US-08-465-590-8	Sequence 8, Appl
10	57.4	0.6	1004	US-08-283-300A-7	Sequence 7, Appl
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12	57.4	0.6	1004	US-08-995-09345-7	Sequence 7, Appl
13	57.4	0.6	1386	US-08-465-590-3	Sequence 3, Appl
14	57.4	0.6	1386	US-08-283-300A-2	Sequence 2, Appl
15	57.4	0.6	1386	US-08-711-417C-3	Sequence 3, Appl
16	57.4	0.6	1386	US-08-998-416-186	Sequence 186, App
17	57.4	0.6	1551	US-08-711-417C-165	Sequence 165, App
18	57.4	0.6	1611	US-08-995-09345-2	Sequence 2, Appl
19	57.4	0.6	5852	US-07-867-106-2	Sequence 3, Appl
20	56.8	0.6	19124	US-08-487-826B-13	Sequence 13, Appl
21	55.8	0.5	615	US-08-998-416-186	Sequence 186, App
22	55.6	0.5	6124	US-08-998-416-595	Sequence 595, App
23	55.4	0.5	6124	US-08-213-419B-3	Sequence 3, Appl
24	54	0.5	7218	US-08-232-463-14	Sequence 14, Appl
25	53.8	0.5	2897	US-08-927-394-1	Sequence 2, Appl
26	53.2	0.5	731	US-08-451-405A-2	Sequence 4, Appl
27	52.4	0.5	3356	US-09-379-523-4	Sequence 4, Appl

28	51.2	0.5	2223	US-08-257-073-4	Sequence 4, Appl
29	50.6	0.5	1128	US-08-465-590-7	Sequence 7, Appl
30	50.6	0.5	1128	US-08-283-300A-6	Sequence 6, Appl
31	50.6	0.5	1128	US-08-711-417C-7	Sequence 7, Appl
32	50.6	0.5	1128	PCT-US95-09345-6	Sequence 6, Appl
33	50.6	0.5	1170	US-08-465-590-6	Sequence 6, Appl
34	50.6	0.5	1170	US-08-283-300A-5	Sequence 5, Appl
35	50.6	0.5	1170	US-08-711-417C-6	Sequence 6, Appl
36	50.6	0.5	1170	PCT-US95-09345-5	Sequence 5, Appl
37	50.6	0.5	1296	US-08-465-590-4	Sequence 4, Appl
38	50.6	0.5	1296	US-08-283-300A-3	Sequence 3, Appl
39	50.6	0.5	1296	US-08-711-417C-4	Sequence 4, Appl
40	50.6	0.5	1296	PCT-US95-09345-3	Sequence 3, Appl
41	50.6	0.5	1788	US-08-465-590-2	Sequence 2, Appl
42	50.6	0.5	1788	US-08-283-300A-1	Sequence 1, Appl
43	50.6	0.5	1788	US-08-711-417C-2	Sequence 2, Appl
44	50.6	0.5	1788	PCT-US93-08743-2	Sequence 2, Appl
45	50.6	0.5	1788	PCT-US95-09345-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-284-782-36
; Sequence 36, Application US/09284782
; Patent No. 6057111
; GENERAL INFORMATION:
; APPLICANT: ENTERPRISES, LTD., GBI
; APPLICANT: Delis, Louis P.
; APPLICANT: Yehely, Fruma
; APPLICANT: Elmova, Elena
; APPLICANT: Vasquez-Iaslop, No. 6057111a C.
; APPLICANT: Elnat, Paz
; TITLE OR INVENTION: GENE IDENTIFICATION METHOD
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kohn & Associates
; STREET: 30500 No. 6057111thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: US
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/284,782
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N
; REGISTRATION NUMBER: 38,972
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-09-284-782-36

Query Match 3.1%; Score 315.4; DB 3; Length 333;
Best Local Similarity 99.7%; Pred. No. 1.3e-67;
Matches 316; Conservative 0; Mismatches 1; Indels 0;

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Query Match      0.74; Score 72.4; DB 2; Length 19124;
Best Local Similarity 49.0%; Pred. No. 2.3e-07;
Matches 257; Conservative 0; Mismatches 256; Indels 11; Gaps 2;

QY 7060 ttaatcagaacaaaccagaagtttggttaacttgggcataatgcaagttactt 7119
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Db 15920 ttaattcatttaatttttttaatttttttttaatttaatttttttttttttt 15861
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QY 7120 tgggcaaaactactcactaagaacaattctctagttgtcggaacaacaattgctttat 7179
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Db 15860 ttttttttttaatttaatttttttttttttttttttttttttttttttttttttt 15801
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QY 7180 ttgggaatgtagtccttttatttcaatcaatttttttttcttcagacaagacag 7239
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Db 15800 attttatgattatatttttttttttttttttttttttttttttttttttttttttt 15749
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QY 7300 accttttagtaaatatatttttggatagcgttcacagatcattatccatcc---tt 7356
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Db 15688 ttttttttttttttttttttttttttttttttttttttttttttttttttttttt 15629
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QY 7357 cttaattatgtaattttatttttcttcttggcttccattatatacatatttggtgg 7416
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Db 15568 atcaaatatttatatttttttttttttttttttttttttttttttttttttttttt 15509
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QY 7477 ttgcacatactaaagcccttatccatctcccaagatataataaattatttttta 7536
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Db 15508 ttttttttttttttttttttttttttttttttttttttttttttttttttttttt 15449
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RESULT 3
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300, 6
; FILING DATE: 26-AUG-1991

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Query Match	0.6%	Score 59.6	DB 4	Length 837
Best Local Similarity	43.9%	Pred. NO.5.6e-05		
Matches 257	Conservative 0	Mismatches 329	Indels 0	Gaps 0

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DB	6	AAATATATATATTTATTAAGATATATATTAACCTTTTATTTATTAATTTATAGT	65

QY 7221 ttcttcagacagacatagtagatcaactagcattggaaaatacatcaactatcttg 7280
DB 66 ATTAAATATTAAACAT 125
QY 7281 gaattatagtgacgctcctctttagaaaatacttttgtagcgttgacagatag 7340
DB 126 CTTAT 185
QY 7341 aattatccactatcttcttattgataattatcttcaatttttgccttcaatt 7400
DB 186 TAAAT 245
QY 7401 atacactcttgctgagagaggttggtgcttttgaagagacaaaattattataa 7460
DB 246 AAAAT 305
QY 7461 cactaacaccccttttgcactataagccttattccactctcgaatataat 7520
DB 306 AAT 365
QY 7521 aaaaattatcttcttcttcttcttcttcttcttcttcttcttcttcttctt 7580
DB 366 TAT 425
QY 7581 cgaactattatgtagcaggaactttcttcaacgaggaattcatgattaggaatt 7640
DB 426 TCAAT 485
QY 7641 ctctctgagaaagcctccctcgtagaagaagatgctgcgcgaatctgctgcca 7700
DB 486 TTTCTAT 545
QY 7701 tttaaaacigaaaatattttaaattatcttctatattcctaaat 7746
DB 546 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 591

RESULT 6
US-09-419-459-1/c
; Sequence 1, Application US/09419459
; Patent No. 6222028
; GENERAL INFORMATION:
; APPLICANT: Liu, Jin-Hao
; APPLICANT: Cheng, Kuo-Joan
; APPLICANT: Tsai, Cheng-Fang
; APPLICANT: Chang, Chia-Chieh
; TITLE OF INVENTION: CELLULOSE ENZYMES
; FILE REFERENCE: 08919/037001
; CURRENT APPLICATION NUMBER: US/09/419,459
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2110
; TYPE: DNA
; ORGANISM: Piomyces rhizinflata
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(1749)
US-09-419-459-1

Query Match 0.6%; Score 59.4; DB 4; Length 2110;
Best Local Similarity 49.9%; Pred. No. 0.0001;
Matches 202; Conservative 0; Mismatches 201; Indels 2; Gaps 2;
QY 7167 atagttcttatttgtagcagtagccttatttcatcaattttttttctct 7226
DB 2108 ATTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2049
QY 7227 cagacagacatagtagtagcagcattggaaaatacatcaactatcttgat 7286

DB 2048 ACAATTTTATATCTTATAGCTATTTAT-TAAATACATATTCATCTTTAAATTC 1990
QY 7287 ttatgtagcgttactcttcttcttcttcttcttcttcttcttcttcttcttct 7346
DB 1989 TTGATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1930
QY 7247 ttccactcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 7406
DB 1929 TTTTATCTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1870
QY 7407 atttgtagaagaggttggtgcttttgaagagacaaaattattataactaa 7466
DB 1869 AATTAATAATTA-AAAATTTTAAATGACATTTTATTTAGAAATATGATATTAATTTTTC 1811
QY 7467 acaactcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 7526
DB 1810 TATTTATTTTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1751
QY 7527 tatttttaattgaagattctgaaattcttcttcttcttcttcttcttctt 7571
DB 1750 TTAACATTTATGACACAAATACATTCATTCATTTTAATTC 1706

RESULT 7
US-08-998-416-1137
; Sequence 1137, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Reblschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYP11
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PR/5-30306/A/CGCI976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8589
; INFORMATION FOR SEQ ID NO: 1137:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 636 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAC1692BP


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RESULT 11
 US-08-711-417C-8
 : Sequence 8, Application US/08711417C
 : Patent No. 6928611
 :
 GENERAL INFORMATION:
 :
 APPLICANT: Georgopoulos, Katia A.
 TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
 NUMBER OF SEQUENCES: 202
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FASTSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/711,417C
 FILING DATE: 05-Sep-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/238,212
 FILING DATE: 02-MAY-1994
 APPLICATION NUMBER: 08/121,438
 FILING DATE: 14-SEP-1993
 APPLICATION NUMBER: 07/946,233
 FILING DATE: 14-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Myers, Louis P.

```

1      REGISTRATION NUMBER: 35,695
2      REFERENCE/DOCKET NUMBER: MGP-027PC
3      TELECOMMUNICATION INFORMATION:
4      TELEPHONE: (617)227-7400
5      TELEFAX: (617)227-5941
6      INFORMATION FOR SEQ ID NO: 7:
7      SEQUENCE CHARACTERISTICS:
8      LENGTH: 1004 base pairs
9      TYPE: nucleic acid
10     STRANDEDNESS: single
11     TOPOLOGY: linear
12     MOLECULE TYPE: cDNA
13     FEATURE:
14     NAME/KEY: CDS
15     LOCATION: 1..1004
16     PCT US95-09345-7

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Query Match	0.68;	Score 57.4;	DB 5;	length 1004;
Best Local Similarity	60.68;	Pred. No. 0.00021;		
Matches 94;	Conservative	0;	Mismatches 61;	Indels 0;
				Gaps 0

[illegible]

RESULT 13590-3
 US-08-465590-3
 ; Sequence 3, Application US/08465590
 ; Patent No. 5824770
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: Georgopoulos, Ktita A.
 ;
 ; TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE

ADDRESSEE: LAIVIE & COCKFIELD
STREET: 60 STATE STREET, Suite 510
CITY: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ascii (text)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,590
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/238,212
FILING DATE: 02-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,438
FILING DATE: 14-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/946,233
FILING DATE: 14-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,695
REFERENCE/DOCKET NUMBER: MPG-006C2DV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1386 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1386
? US-08-465-590-3

Query Match 0.6%; Score 57.4; DB 1; Length 1386;
Best Local Similarity 60.6%; Pred. No. 0.00025;
Matches 94; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4284 aaatgtgtcactgtgcatctgtcttcgtgatgaatgatagtatgcatcttgcatatagt 4343
DB 1213 AAGTGGCAACACTGCCGGGTGCTCTTCCGTGATCAGTCATGTACACATCCACATGGGC 1272
QY 4344 tgcacatgtgacagtgacatttcacatgacacatataccacagcatcttgcacggacaa 4403
DB 1273 TGCCACGGCTTCGTCATCTTTGAGTGCAACATGTGGCGCTACACAGCCAGGACCGG 1332
QY 4404 tatgacttcacacacatatccagagggcctgca 4438
DB 1333 TACGAGTTCGTGCGACATTAACGGAGGAGGACGA 1367

RESULT 14
? Sequence 2, Application US/08283300A
? Patent No. 6172278
? GENERAL INFORMATION:
? APPLICANT: Georgopoulos, Katia A.
? TITLE OF INVENTION: IKAROS TRANSGENIC CELLS AND ANIMALS
? NUMBER OF SEQUENCES: 26
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: LAHIVE & COCKFIELD
? STREET: 60 STATE STREET, Suite 510
? CITY: BOSTON
? STATE: MASSACHUSETTS
? COUNTRY: USA
? ZIP: 02109
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII (text)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/283,300A
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/238,212
? FILING DATE: 02-MAY-94
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/121,438
? FILING DATE: 14-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/946,233
? FILING DATE: 14-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Myers, Paul L.
? REGISTRATION NUMBER: 35,695
? REFERENCE/DOCKET NUMBER: MCP-027
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (617)227-7400
? TELEFAX: (617)227-5941
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1386 base pairs

? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1386
? US-08-283-300A-2

Query Match 0.6%; Score 57.4; DB 4; Length 1386;
Best Local Similarity 60.6%; Pred. No. 0.00025;
Matches 94; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4284 aaatgtgtcactgtgcatctgtcttcgtgatgaatgatagtatgcatcttgcatatagt 4343
DB 1213 AAGTGGCAACACTGCCGGGTGCTCTTCCGTGATCAGTCATGTACACATCCACATGGGC 1272
QY 4344 tgcacatgtgacagtgacatttcacatgacacatataccacagcatcttgcacggacaa 4403
DB 1273 TGCCACGGCTTCGTCATCTTTGAGTGCAACATGTGGCGCTACACAGCCAGGACCGG 1332
QY 4404 tatgacttcacacacatatccagagggcctgca 4438
DB 1333 TACGAGTTCGTGCGACATTAACGGAGGAGGACGA 1367

RESULT 15
? Sequence 3, Application US/08711417C
? Patent No. 6228611
? GENERAL INFORMATION:
? APPLICANT: Georgopoulos, Katia A.
? TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE
? NUMBER OF SEQUENCES: 202
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Fish & Richardson P.C.
? STREET: 225 Franklin Street
? CITY: Boston
? STATE: MA
? COUNTRY: USA
? ZIP: 02110-2804
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: Windows 95
? SOFTWARE: FASTSEQ for Windows Version 2.0b
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/711,417C
? FILING DATE: 05-SEP-1996
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/238,212
? FILING DATE: 02-MAY-1994
? APPLICATION NUMBER: 07/946,233
? FILING DATE: 14-SEP-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Myers, Louis P.
? REGISTRATION NUMBER: 35,965
? REFERENCE/DOCKET NUMBER: 10287/007001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617/542-5070
? TELEFAX: 617/542-8906
? TELEEX: 200154
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1386 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:

NAME/KEY: Coding Sequence
LOCATION: 1...1383
SEQUENCE DESCRIPTION: SPQ ID NO: 3:
US-08-711-417C-3

Query Match 0.68; Score 57.4; DB 4; Length 1386;
Best Local Similarity 60.68; Pred. No. 0.00025;
Matches 94; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 4284 aaatgtgtgactgtggcatgtcttctcgtgatgaagatgtatgtcttgcatatgagt 4343
DB 1213 AAGTGGGAACACTGCCGGGTCTCTCTGATCAGTATGATACCATCCATGAGGC 1272
QY 4344 tggcatgtgacagtggaccccttccaggtgacatatgccagcatctttgacgacaaa 4403
DB 1273 TGGCAGGCGCTTCCGTCATCTTTTGAAGTGCACATGTGGGGCTTACACAGCCAGGACCGG 1332
QY 4404 latgactlcaacacatalccagaaggccctaca 4438
DB 1333 TACGAGTTCTCTCGCACATACGCCGAGGGGAGACA 1367

Search completed: July 21, 2002, 21:27:49
Job time: 22556 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 14:53:23 ; Search time 6987.25 Seconds

(Without alignments)
19925.019 Million cell updates/sec

Title: US-09-702-216-1
Sequence: 1 ttctccgcgaagctcctt.....gttatttcaaaaaaaaaa 10315

Scoring table:

IDENTITY_NUC
Gapop 10.0 ; Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estlin.*
4: em_estlinu.*
5: em_estlov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	879.8	8.5	928	9	AL565773
2	837.2	8.1	842	9	AL535097
3	722	7.0	810	10	BI825385
4	713.4	6.9	824	10	BG254038
5	703.4	6.8	792	10	BI664283
6	693.2	6.7	765	10	BI596760
7	690	6.7	783	9	AV687506
8	681.6	6.6	691	9	AV687506
9	656.6	6.4	742	9	AV687506
10	652.8	6.3	886	10	AV687506
11	649.2	6.3	1043	10	BI686434
12	649	6.3	649	10	BI686434
13	648.6	6.3	813	9	BI92548
14	630	6.1	649	9	BI92548
15	629.4	6.1	679	10	BI92548
16	607.8	5.9	740	12	AG186896
17	606.8	5.9	650	9	BB641330

C 18	599.2	5.8	728	10	BI106944
19	594.8	5.8	598	9	AW303579
20	592.2	5.7	964	10	BI115118
21	578.2	5.6	917	10	BI178176
22	576.2	5.6	953	10	BI138096
23	571.8	5.5	602	12	AG025673
24	569	5.5	569	9	AW021592
25	567.8	5.5	749	10	BI139707
26	547	5.3	547	9	BI139707
27	546.4	5.3	584	9	AW973691
28	544.4	5.3	661	10	BI152146
29	541.6	5.3	569	9	AW021592
30	541.4	5.2	543	9	AW021592
31	539.8	5.2	567	10	BI152146
32	539.8	5.2	1028	10	BI082772
33	536.8	5.2	925	10	BI082772
34	531	5.1	729	10	BI168531
35	529.4	5.1	732	10	BI168531
36	529	5.1	542	9	BI168531
37	525.2	5.1	673	9	BI168531
38	525	5.1	525	10	BI168531
39	520.8	5.0	560	9	BI168531
40	520.2	5.0	566	9	BI168531
41	517	5.0	528	9	BI168531
42	513.6	5.0	521	9	BI168531
43	505.6	4.9	847	10	BI139728
44	503	4.9	503	9	AW070915
45	502	4.9	667	10	BI174562

ALIGNMENTS

RESULT 1	AL565773	928 bp	MRNA	linear	EST 16-FEB-2001
LOCUS	AL565773/c				
DEFINITION	AL565773 LTR-FL013-FRml Homo sapiens cDNA clone CS0DF008Y101 3				
ACCESSION	AL565773				
VERSION	AL565773.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polyes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
CONTACT	Contact: Genoscope				
Genoscope	- Centre National de Sequencage				
BP 191 91006 Evry cedex - France					
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.					

FEATURES

1..928	Location/Qualifiers
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone="CS0DF008Y101"	
/clone_lib="LTR-FL013-FRml"	
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"	
/lab_host="DH10B"	
/note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"	
BASE COUNT	319 a 164 c 148 g 280 t 17 others

ORIGIN

Query Match 8.5%; Score 879.8; DB 9; Length 928;
 Best Local Similarity 96.4%; Pred. No. 1e-123;
 Matches 895; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

QY 7634 gaatttcctcttggaagagcctcccttgatgaatgagatgagcgaataatg 7693
 DB 927 GGAAATTCCTCTTGGAAGAGCGTCCCTGCATGAAATGATCATGCCAGCTAAATTC 868
 QY 7694 lgtgcattttaaactgaaatattttaaattatgtctatatttcaattagctt 7753
 DB 867 TGTGCATTTTAAATCTGAAATATTTTAAATTTTGTCTATATTTCAATTAATGAGCTT 808
 QY 7754 tggatcaactttaggcaggacagcagctcgtctcattccctcccttccacttt 7813
 DB 807 TGGATCAAACTTTAGGCCAGACACCATTCGCTTCATCTCTCTCTTTCTCACTCTT 748
 QY 7814 tctctcactcaccctcgtatcattcctgttcttgagatgaaatcatalaagagc 7873
 DB 747 TCTCTCATCTCACTCACTCTCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 688
 QY 7874 caaccacatcagaacgltgtgattgagagagacatcagcagcagatattgaga 7933
 DB 687 CAACCCATCTCAGAGAGTGTGTGATGAGAGAGACTACATGACTCCAGATATAGAGA 628
 QY 7934 aaagagagagctcctaactgataactcgtatgctcaaaaggaagagatgcccaatc 7993
 DB 627 AAAGAGAGAGCTCTTAATGATTAATCTGTAGTTCAAAAGAGAAAGATGCCAATTC 568
 QY 7994 tctctcagacatattgagattttttttaaacttttaagaatgagatgctcgtc 8053
 DB 567 TCTCTACATGACATATTGAKATTTTAAATCAATTTTAAATAGTACATCTCTCTCT 508
 QY 8054 taaactgtcgttttagtgaagtagattttttaaacaagacalggagagatttct 8113
 DB 507 TAACTGTCTGTTTATGAGAGTAGATTTT-TAAMCAGACATGGGAGATCTTTTCT 449
 QY 8114 aaggttaatttaaggaaggaagaaagratcctttaaagagctcttcttgagagcgtg 8173
 DB 448 AAGGTATATTAATGAGAGVMAAAAGATATCTTAACAGCTCTTTGTAAMCCTGTG 389
 QY 8174 gaaacattatgttataatttgcaatgagacatataactatattatgacaaatgaaat 8233
 DB 388 CTACACATTAATGTTTATTAATGACATGTCACATTAATCTATTAATGATCCAAATGCA 329
 QY 8234 acagctccaaaatataatgatalatattttaaagccttgaggaataatcttctc 8293
 DB 328 ACAGCTCCMAAAATATTAATGATATATTTTAAATGCTGTGAGAAATACATTTTCTC 269
 QY 8294 ttaataactggaagctcagtgatgctttaaataattatgagcctcctgtgtgtg 8353
 DB 268 TTAATATACTGAGAGGCTCAGTATGCTATTAATAATATTAATGATGCTCCTGTGTGTG 209
 QY 8354 gctgcaaaacatcacaaagtgaccggtcttgagagactgtgagacgtgagcctgtttagta 8413
 DB 208 GCTKCAAAACATSAACAAGTACCGGCTTGTGACACTGTGTGAATCTGTGCTGTGTTAGTA 149
 QY 8414 aataaaatgaatgcatlcttagaaggggaatatctccatcgaagtgaggaatgagag 8473
 DB 148 AATTAATTAATGAATCTTCTAGAGGGGGAATATCTCCATCCAGGTGGAAATGTGGAG 89
 QY 8474 taaagaagctggt 8533
 DB 88 TAAAGAGCTATCTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 8533
 QY 8534 aggtcaactttagctacgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 8561
 DB 28 AGTCAACTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 1

RESULT 2

AL535097
 LOCUS AL535097 842 bp mRNA linear EST 13-FEB-2001
 DEFINITION AL535097 L7L1_F1013_FBrn1 Homo sapiens cDNA clone CS0DP008Y101 5
 prime, mRNA sequence.
 ACCESSION AL535097
 VERSION AL535097.1 GI:12798590
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 Li W.B., Gruber,C., Jesse,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 CONTACT: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. 842
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DP008Y101"
 /clone_11b="L7L1_F1013_FBrn1"
 /dev_stage="pooled tissue from post conception fetuses (20
 week, 24 week and 26 week)"
 /lab="host="DH10B"
 /note="Organ: Fetal brain; Vector: pCMVSPORT 6; 1st strand
 cDNA was primed with a Molli-Oligo(dT) primer. Five prime
 end enriched, double-stranded cDNA was digested with Not I
 and cloned into the Not I and Eco RV sites of the
 pCMVSPORT 6 vector. Library was constructed by life
 technologies. Contact : Peng Liang liang.technologies, a
 division of Invitrogen 9800 Medical Center Drive Rockville
 , Maryland 20850. USA. Fax : (1) 301 610 8371 Email :
 liang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 249 a 130 c 126 g 337 t
 ORIGIN

Query Match 8.1%; Score 837.2; DB 9; Length 842;
 Best Local Similarity 99.6%; Pred. No. 3e-117;
 Matches 839; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7090 aacttggacaatgacaagtattacttcttggcaaacactaactaagaattctc 7149
 DB 1 AACTGGGCAATATGACAGATTAATCTTTTGGCAAACTACTCATTAAGCAATTTCTC 60
 QY 7150 tagtgtctggacaacaatagttcttatttttgagatgagccttatttcaatc 7209
 DB 61 TAGGTGTGCGACACAAATAGGCTTCTTAATTTTGGCATGATAGCTTTTAATTTTCAAT 120
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 QY 7270 caactatcttggaaattatgtatgctcacttttagttaaatttttggtagcgt 7329
 DB 181 CACTATCTTGGAAATTTATGAGTACGACTTTTATGTAATAATTTTGGATAGCCGT 240
 QY 7330 tgaagatagatcttatcactccttattattatgataattatttatttcttctt 7389
 DB 241 TGACACATAGATCTTAATCACTCTTTTAATTTATGTAATTTTAATTTCAATTTTGG 300
 QY 7390 ctctcatattataactatttttggltggaagaggttggccttttttgaagagacaaa 7449
 DB 301 CTTTCATTAATTAATTAATTTTGGTGGAGAGAGGTTTGGCTTTTGAAGAGACAAAA 360
 QY 7450 atttattataacactaaacactccttlttggacatttaagccttattcactccta 7509
 DB 361 ATTATATATAACACTAAACACTCTTTTGGACATTAAGACCTTATTCACATCTCTCA 420

Accession	Sequence	Length
Oy 7510	aaatcatalaataatcatttttaacttaagcttcgaattatcttaaat	7569
Db 421	acatvtatvtatataatatttttttaattttacgatttcgaatttttttcgttaatt	480
Oy 7570	gtagatttaacagagctatctgttcggaacttttttaabagaatttcagat	7629
Db 481	ggatttttaaacagcgtatvtgtctacgaaatttttttattagagatttcattgatt	540

541 TTAGGATTTCTCTCTCTGGAAGGCTTCCCTGTGANGAATGATGTGCCAGCTAAA 600

Db 601 ATGTGTGCCATTTAAACGGAATAATTTAAATTTTCTCTATTTCTTAATTCGA 660

Db	661	GCATTGATCAACATTAGGCCAGSACGCTCATGCGTCTCATTTCTCTTTTCTCAC	720
Qy	7810	tcctctctcattcactcaccctctgattcaattcctttggttggatagaaaaatcatana	7869

Db	721	TCCTCTCTCATCACTCACCTCTGATTTCATTCCTGTTCTTGGATAGAAAAATCATAAA	780
Qy	7870	gaaccaaccatctcagaacgtlglgattlgagagagacactatagactccaagtatat	7929

DO 781 GAGCCAAUCCATCTTCAGAACTTGTGGATTGAGAGAGACACTCATGACTCCAGATAT 840
 QY 7930 ga 7931
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RESULT 3

LOCUS	B1825385	810 bp	mRNA	linear	EST 04-OCT-1998
DEFINITION	603072307F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5164584 5'				
ACCESSION	mRNA sequence.				
	R1825385				

FUNCTION	B1825350.1	G1:12930355
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 810)
NIH-MGC <http://mgc.ncl.nih.gov/>.

JOURNAL
 unpublished (1999)
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

http://image.lnl.gov
Plate: L1AM1408 row: m column: 01
High quality sequence start: 5
High quality sequence stop: 806

source	location/qualifiers
1. 810	/organism="Homo sapiens" /db_xref="taxon:9606"

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/clone_id="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"

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/note=Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and

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directionally cloned (XbaI site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH-MGC Library." 250 a 203 c 181 g 176 t

Query Match	7.0%;	Score 722;	DB 10;	Length 810;
Best Local Similarity	96.9%;	Pred. No. 8	6e-100;	
Matches 789;	Conservation	0.0	Wisc	1.0

[illegible]

Dy 3326 tgcgaattgcttgaccacaagaacccctcctctcggaagaatgtaatlqggagatatgt 3385
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 tgccaatttggcctgaccaccaaacctctctcttcgcccaagaatgcaaatggcgcatatgct 119

QY 3386 atgcaacgctgtgtgcccctaccagaagcttcaactccacagcctttaacatcat 3445
 |||||
 Db 120 ATGCAACGCTGTGGCCCTTACCAGAACTTCACTGACTGCCAGGCCTTAAACATCAT 179
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Db 180 TAAACAAACACCGTGAGCAGTTATTAGGAGGAAACAGAAAGCGCTTAACCCAGA 239

[illegible]

Db	300	TGGAAGCCCGTTAGAGAGAGGTCAGAGATCATCTAACTGAAAGTCACACAGAGAAAT	359
Q7	3626	tcacatcccacgcctaagtaagtagcaagcccaagattcattagcctaaaaacccattctcc	3695

QY	3686	tcagcagccagtcctgtgcagcccaactcgtgatatctcaaaaagatgcacacttgcga	3745
Dd	360	TCCACTCCCCAGCCTAAATAATACGAGCCCA-GGTTCAATTGACTAAAGCATTTCTGC	418

DB	419	ICAGGAGCGAGTCTCTGGTCAGGCCAAACTCTGGATATTTCACAAAAGATCCAACTTTTGA	478
DQ	3746	cattcagataaaaagttccctcagaagaagtactgtgagatccagaatatgttcacgcatc	3805

QY 3806 tgaagggaaggaagttcttgagagagcagttcctatagaaagttacatgagacctcgaa 3865
|||||

QY 3866 acaccocaaattatcaccaccagcgagccctattgaaaagtaccagttaccacttttgg 3925
|||||
500 acaccocaaattatcaccaccagcgagccctattgaaaagtaccagttaccacttttgg
|||||

OY 3926 actccctttgtacataatgaacttccagagtgaagctgattgctgcgttcrgagtaa 3985
|||||
658 ACTTCCCTTTGTACATATGACTTCAGAGCGAAGCTGATTGGCTGCAGCTTTCGCTCCT - 716

Qy 3986 atataagctctcgttccgtggaatccgcactacttgatgaatcgtgctgacctaccaa 4045
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Db 717 ATATAGCTCTCGTTCCTGGGAATCCGCACTACTTGAATCAGATGCTGTGGCTACCAAA 776
|||||

QY	4046	tccctggc-aaactatgtgccttatccacoclt	4078
Dd	777	TCCTTGCCAAAAAAGTATGTGCTTATCCCACCTT	810

RESULT 4

LOCUS BC254038 824 bp mRNA linear EST 13-FEB-2001
 DEFINITION 60236675F1 NIH_MGC_91 Homo sapiens CDNA clone IMAGE:4475131 5',
 mRNA sequence.
 ACCESSION BG254038
 VERSION BG254038.1 GI:12763844
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 824)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: DCM/DMP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM10300 row: e column: 20
 High quality sequence stop: 699.

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4475131"
 /clone_lib="NIH_MGC_91"
 /tissue_type="adenoecarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: prostate; Vector: pCMV-SPORT6; Site:1: NotI;
 Site:2: SalI; Cloned unidirectionally; oligo-dt primed.
 Average insert size 1.4 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH-MGC library."

BASE COUNT 265 a 205 c 180 g 174 t
 ORIGIN

Query Match 5 9%; Score 713.4; DB 10; Length 824;
 Best Local Similarity 95.2%; Pred. No. 1,7e-98;
 Matches 766; Conservative 0; Mismatches 36; Indels 3; Gaps 3;

QY 3397 gggccctaccgaagctcactgcagctccgaagcttaacatgaatgaacaaaca 3456
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 Db 6 GTGGCCCTTACGACGAACTTCACCTCCGACGCTTTAAACATCATTAACAAACA 65

QY 3457 acggtgacagattatgaagagagaaagacgcttaaccagaagcactcaag 3516
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 Db 66 ACGGTGGACGATTATTAGAGAGAGAAACAAAGCGCCTTAAACGAGGCACTTACG 125

QY 3517 ctgagcagctcaacaaacagcagcagcagcagcagcagcagcagcagcagc 3576
 |||||||
 Db 126 CTGAGCAGCTCAACAAACAGAGAGGCGCAGCATAGAGAGCAGCATGAGAGCCCGT 185

QY 3577 taagagagagtcagaagatcatcctaagtcagcagcagcagcagcagcagc 3636
 |||||||
 Db 186 TAGAGAGAGAGTCAGAGATCATCTAAGTAAAGTCAACAGAGAAATTCACCTCCA 245

QY 3637 gccctaagtaatacgaagcccaagggtcattgactaataaagccattctgca 3696
 |||||||
 Db 246 GCGTAAGTAAATACGAAGCCCGAGGTTGACTTAAAGGCATTCCTGACAGAGCAG 305

QY 3697 tccgtgtaagccaactctgatatctacaaagagtgaaactctgcaatcagata 3756
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 Db 306 TCCGTGACAGCCAACTCTGGATATTCACAAAGAGATGCAACCTTGCACATTCAGATA 365

QY 3757 aaagtcctcagaagagctcgaagatccagaagaaatgctatccgttcgaagga 3816
 |||||||
 Db 366 AAAGTCCTCAGGAAGTACTGAGATCCAGAAATAGTTCAATCCGTATCGAAGGGAAG 425

QY 3817 gaagtcctcagaagagcagctcctatagaanaagtaatgagacctcgaacacccaalt 3876
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 Db 426 GAAAGTCTGAGAGAGCGAGTCTATGAAAAAGATGAGCATGAGACGCAACACCAAAAT 485

QY 3877 attcaccacagcagcagcctattgaaagtaaccagtaaccacttttgagctcccttg 3936
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 Db 486 ATTCACCCACAGCGCAGCCCTATTGAAAGATACACACCTTTCGACCTCCCTTGG 545

QY 3937 tacataatcactcagaagtagaagcagctgagctcggcttcgagtaataataaact 3996
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 Db 546 TACATTAATACCTTCAGAGATGACGATGATGCTGGGCTTGAGAT-AAATTAACCTCT 604

QY 3997 cggctcct-gggaatccgcactacttgagtcagcagtcgctggcctacaactccctca 4055
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 Db 605 CCGTCTCTGGGAAATCCGCACTACTGATGACAGGCGCTGGCCATCCAAATCTTGCCA 664

QY 4056 aactatggccttaccacctcactcactcgtcctcctatctttagctgttgatcagac 4115
 |||||||
 Db 665 AACTATGTCCTTATCCACTTTCAATGCTCAATTTCCACCTCTTGATCAAGA 724

QY 4116 aatgacattcctcagatttggcagatcagacatccagcctgggccaactgcaacgt 4175
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 Db 725 CAATGAATTCCTCTGATTTGGATTCACGATACCAAGACTGGG-CAACTCAAACTGT 783

QY 4176 gctccaagagagaaacgaagcacc 4202
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 Db 784 GCCTCCAGAGAAAGACGACACACCA 810

RESULT 5
 B1664283 792 bp mRNA linear EST 12-SEP-2001
 LOCUS B1664283
 DEFINITION 60328903F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5323113 5',
 mRNA sequence.
 ACCESSION B1664283
 VERSION B1664283.1 GI:15578516
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 792)
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: c9apbs-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LLM1819 row: j column: 10
 High quality sequence stop: 791.

FEATURES
 source
 1..792
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5323113"
 /clone_lib="NCI_CGAP_Mam6"
 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
 Site:2: NotI; Cloned unidirectionally. Primer: Oligo dT.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 237 a 191 c 172 g 192 t

ORIGIN

Query Match 6.8%; Score 703.4; DB 10; Length 792;
 Best Local Similarity 94.6%; Pred. No. 5.7e-97;
 Matches 750; Conservative 0; Mismatches 41; Indels 2; Gaps 2;

3590 agaagatcactactgaagatccacagagaagaatccaactcccagctaataa 3649
 1 AGAAGATCACTTAAAGTGAAGATCCAGGAAGATTCACCTCCGAGCTGAGTAATA 60

3650 cgaagccagggttactactaaagccattctgctcagcagccagcccggtcacca 3709
 61 CCAAGCCAGGTTCACTTACTTAAAGCCATTCTGCTCAGCCAGCTCGTGGTACCA 120

3710 aacttgataltcaaaaaaggatgcaacctttgacacatcagataaaag tccctcaga 3769
 121 AGCTGTGATATCCACAAAGATCCAGCTTTGCACTTCAGATAAAAGTCTCTCAGGA 180

3770 aagactggagatccaggaataatgttcatccgtatctgaagggaagaagttctgagag 3829
 181 AAGTACTGAGATCCAGGAAGATTCATCCGATCTGATGGGAAGGAGACTTCTGAAG 240

3830 aggcagtcctatagaagaatgaatgagacctgcaaaaccccaaatattacacacagag 3889
 241 AGGCAGGCCCATGCGAAAGTACATGAGACCTGCAAAAACCCCACTATTCTCCACAGC 300

3890 cagccctaltgaaaaaglaacaglaacccatttttgacctcccttgatcataatgacctt 3949
 301 CAGCCCATGCGAAAGTACCAATACCCGTTTTTGGAGTCTCTTGGTACATTAATGACTT 360

3950 ccagagtgagagctgattggcgcggttcctggagtaataataagctctcgttctggagaa 4009
 361 CCAAGTGAAGCTGATGGCTTACGCTTCTGGAATTAATTAAGCTCTCCGTTCTCTGGGAA 420

4010 tccgcactacttgaagtcagtcgctggcctcaccacaaatctctgcaaaatagtggcctta 4069
 421 TCCGCACACTGATGAGTCAATGCTGCTGCTTACCAAACTCTTCCCAAACTATGCTCTTA 480

4070 tccacacttcaatctgctcctcctcaatlttcaagctgttgatcaagaacaatgacctctt 4129
 481 TCCACACTTCAATCTGCTCCTCCATTTCTCAGCTGTGGATGAGCAATGACATTCCTCTG 540

4130 agtttgggagatcaagcatctccagacctgggccaactgtcaaacggttgcctccaagagaa 4189
 541 AGATTGGGATCAAGCATCTCCAGACCTGGGCCCACTGCAAAATGCTGCTCTCCAGGAGAA 600

4190 aacgaagcagcaccacaatgttaaaa-aatgaaggtcccttgatgtatgaaacagagaa 4248
 601 AACGAAGCAGCACCACTGTAAACATGAAGTCCCTTGATGATGATTAACGAGAGAA 660

4249 aagtlgatagaaglaactcaagaatgaaacttcaacaaatgtgtgactgtgacatgtctt 4308
 661 AAGTGAAGAGAGCACTCAAGATGAACTTTCACGAAATGTGTGACATGTGGCACTTGT-A 719

4309 ttctgataaagtgatgtatgtcttgatatagtggttgcacatgggagagagacgttctcc 4368
 720 TACTGGATGAAGTGAATGATGCTTTCGATATGATGTTGCCATGAGTGAAGTGAAGCTTCTCC 779

4369 agtgcagcatatg 4381
 780 AGTGCAGCATATG 792

RESULT 6
 B1596760 765 bp mRNA linear EST 07-SEP-2001
 LOCUS 603242844P1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5285410 5',
 DEFINITION mRNA sequence.
 ACCESSION B1596760
 VERSION B1596760.1 GI:15489699
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 765)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-r@mail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraiki
 Yoshiyuki and Piero Carninci (RIKEN)
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: L14M1721 row: 9 column: 11
 High quality sequence stop: 764.
 Location/Qualifiers

COMMENT

1. 765
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5285410"
 /clone_lib="NIH_MGC_96"
 /issue_type="hypothalamus"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pBluescriptR (modified
 pBluescript KS+); Site:1: BamHI; Site:2: SalI-XhoI (gtagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTNN-3',
 size-selected for average insert size 2.3 kb and
 normalized to R0F 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NHGRI, National
 Institutes of Health). Note: This is a NIH_MGC Library."
 BASE COUNT 237 a 132 c 148 g 247 t 1 others

FEATURES

source

Query Match 6.7%; Score 693.2; DB 10; Length 765;
 Best Local Similarity 98.6%; Pred. No. 2e-95;
 Matches 752; Conservative 0; Mismatches 4; Indels 7; Gaps 5;

ORIGIN

7755 ggaatcaactttagggcagagcacaagcctcaagcgttccattcttcttccactt 7814
 4 GGATCAAACTTAGGCCAGGACCACTCATGCG-TCTCATCTCTCTTCTCATCTCTT 62

7815 ctctcatcactcaacctctgtattcatctctgtgttggtgagatagaataatcataagagcc 7874
 63 CTCTCATCACTCACTCTGTATTCATCTCTGTGTGGATGAGAAATCATTAAGAGCC 122

7875 aaccatctcaagaagctgttgatgagagagacactcaactgaactccaaatataagagaa 7934
 123 AACCATCTCAGAACCTGTGATTTGAGAGAGACATCACTCCAAAGATATGAGAA 182

7935 aaggacagagcttaattgataactctgttgatgaaagaagaagaatgagatccaatctc 7994
 183 AAGGACAGAGCTTAATTATTAATCTGTGTTTCAGAAAGGAAAGATATGCCAAATCTC 242

7995 ctctacatgacatatgagattttttaaactcaactttaaagatgattgtctgtct 8054
 243 CTCTACATGACATATGAGATTTTAAATCAACTTTAAATGATGATGATGATGATGATG 302

8055 aaactgttctgtttagtgaagtagatatttataaacaagaacatgggattcttctcta 8114
 303 AAATGTTCTGTTTAAAGTGAAGTATGATTTTAAACAAACATGGGATCTTTTCTTA 362

8115 aggtatattataagaagaagaagaatattttaaagcctcttgttgaagcctgttg 8174
 363 AGGTAAATATTAAGAGAGGAGAAAGATATCTTTTAAAGACTCTTGTGTAAGCTGTGG 422

8175 tagcacatatgttataatgacatgtgacataatctatattatgacatgcaata 8234

|||||
Db 423 TAGACATATATTTATATATGACATGTCACATATATATATGATCCCAATGCAATA 482
Qy 8235 cagctccaaaataataaagatataataataaagctggggaataactttct 8294
Db 483 CAGCTCCAAAAT 542
Qy 8295 laataaactgaagctcagatagcctataataataatattagcctcctgtgtgtg 8354
Db 543 TATTAATAAGTGAAGCTGTCAGTATGCTATATATATATATATATATATATATATAT 602
Qy 8355 ctgcaaacatcacaaagtgacagcttggaagcctgtgaacgtgtgcctgttaagtaa 8414
Db 603 CTGCAAAACATCACAAAGTACCGGTCTTGAGACCTGTGAACCTGCTGCTTTAGTAA 662
Qy 8415 ata-aatlaagcattcctcagagggg---aatactgcacacagtggtgaagtgtg 8470
Db 663 ATACAAATATATGATTTCTAGAGGCGGCAATTTCTGCGCATCCAGTGTGTAATGTG 722
Qy 8471 ga-gtaagaagctgt 8511
Db 723 GAGCTAAAGAGCTGT 765
RESULT 7
AV687506 783 bp mRNA linear EST 16-JAN-2002
LOCUS AV687506 GNC Homo sapiens cDNA clone GKDRB04 5', mRNA sequence.
DEFINITION AV687506
ACCESSION AV687506
VERSION AV687506.1 GI:10289369
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,
Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
TITLE Insight into hepatocellular carcinogenesis at transcriptome level
with those of corresponding noncancerous liver
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
COMMENT 21625106
CONTACT: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex. 45)
Fax: 86-21-50801922
Email: hanzg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Source
1..783
Location/Qualifiers
/organism="Homo sapiens"
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/clone="GKDRB04"
/clone_1id="GNC"
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/dev_stage="Adult"
/lab_host="SOLR"
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XhoI"
BASE COUNT 256 a 143 c 152 g 230 t 2 others
ORIGIN
Query Match 5.78; Score 690; DB 9; Length 783;
Best Local Similarity 95.28; Pred. No. 6, 1e-95;
Matches 756; Conservative 0; Mismatches 27; Indels 11; Gaps 4;
Qy 4445 caatgacaagtggaaaataaactgaagaagataaacttgacactgaagacaa 4504

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Db 1 CAATGACAGGGGGAGAAAATGSAAAACCTTAAGAGTAAACCTTGACATTAGCACA 60
Qy 4505 ttaataagaataggtttctcttgatggaatcaatagctgttaagtcttataagacc 4564
Db 61 TTAATAGAAATAGGTGTCTGTATGAGAAATCAATACCTTGTAATGTCTTATGAGAAC 120
Qy 4565 taataaaaataactcatalagagcgtcttaccacatgaatattccctctlltgta 4624
Db 121 TATTAATAAAATATCTTCAVWAGAGCTGCTTATCCACACATGAAATTCCTTTGTG 180
Qy 4625 ttctttcttgatgaggttgatccagatataaagaatgaatgaatgaatgaatgaatga 4684
Db 181 TTTCTTTCTTTTATGATGAGTTTACCAATATTAATAAGTGAATTAATGCTCATAGAGA 240
Qy 4685 agaatagaatagtgtaacaatacactttaaacccttgtaagtcaaacaccacttggt 4744
Db 241 AGAATGGAAGATGTGGAACCAATCACTTTAAACCTTTATAGTCAAAACCAATCTTGCT 300
Qy 4745 aatagtactggggaataatcatalaagaatatacacaactagaatlaatalat 4804
Db 301 AATATGTACTGCGCAAAATCAATCAATGAGATATCACACAGCTGATTAATATTTAT 360
Qy 4805 aagaagaagacccaactgtctagaattgaaggtttacataataataaagc 4864
Db 361 AAGAAAGAGACCAAACTGTGATGATTTGAAGGGGTTCATATATATATATATAGCA 420
Qy 4865 agtactggactgtgcatcttgacattgttccaaacacataaattgttgcttaatta 4924
Db 421 AGTACTGGACGGCCATTTGACCATATGTTCCAAACCCATTAATGTTGCTTAATTTA 480
Qy 4925 taatgataataaacctcagaagaggaagaatgaagctccagagcaatgaaga 4984
Db 481 TATATGATCATGAACCCCTATGACAGAGAGAGAAATGAAGGTCCACGGCATGAAAG-- 538
Qy 4985 aatggcgccctcacaattagctctctcattggccagatttgcactaga 5044
Db 539 --ATGGCCCTCTCAATTTAGACTTCTCTCAATGGCCATGTGAGATTGACCT-- 593
Qy 5045 aatgagactgt 5104
Db 594 ATTGGACCTGT 653
Qy 5105 gctgttttaccagccctgt 5164
Db 654 GCTGTTTACCCAGACCTGCTGTACAWACACATGACACCCCTCTGATGATTTTGC 713
Qy 5165 cttagatgttcaaatlacatagatccttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 5224
Db 714 CTTTAGATGTTCT--TACTCAGTAGTCTCTGTTTGGGNTTATGATCATTTGT-CAC 769
Qy 5225 acatgtaccattt 5238
Db 770 ACATGTACCCATT 783
RESULT 8
LOCUS AUI17444 691 bp mRNA linear EST 19-OCT-2000
DEFINITION AUI17444 HEMBA1 Homo sapiens cDNA clone HEMBA101411 5', mRNA
sequence.
ACCESSION AUI17444
VERSION AUI17444.1 GI:10932413
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 691)
AUTHORS Oda, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S., and
Ishigai, T.
TITLE HRI human cDNA project

JOURNAL
COMMENT

Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

source

Location/Qualifiers

1..691
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/db_xref="taxon:9606"
/clone="HEMBA1001411"
/clone_lib="HEMBA1"
/tissue_type="whole embryo, mainly head"
/dev_stage="embryo, 10 weeks"
/note="Vector: pME185FL3"
BASE COUNT 211 a 93 c 104 g 280 t 3 others
ORIGIN

Query Match 6.6%; Score 681.6; DB 9; length 691;
Best Local Similarity 99.0%; Pred. No. 1.2e-93;
Matches 684; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 6988 taatttcttagtaaaagaataacagaatgcacgtgcgaatccttaagaacataatc 7047
|||||
Db 1 TAATTTCTTAGTAAAGAAATACGAATGCATCGTGGCAATCGTTAAACCAACTTATTC 60
QY 7048 tatgtgacgtcgttaaatcagcaaaacacagaaagtttgatlaacttggacataagaca 7107
|||||
Db 61 TAAATGTCACGCTTAAATCAACAAACACCAAGTTGGCTTAACCTCCGCAATTAACGACA 120
QY 7108 agtatactcttttggcaaaactactcaatcaatctctcagtgtgtggacacaa 7167
|||||
Db 121 AGTATTACTTTTGGCAAACTACTCTTAAGCAATTTCTGATGTCGGACACAA 180
QY 7168 taggttcttatttttggacatgatagccttttatttcaatcaattttttttttttttc 7227
|||||
Db 181 TAGGTCCTTAATTTTGGCATGATGCCCTTATTTTCAATTCATTTTCTTCTC 240
QY 7228 aagaagacatagatatacaactacatgataagaaatacalatcaatcttllgaaatatt 7287
|||||
Db 241 AGACGACATAGTAGTAGACTACATTCGAAATACATATCATTTCGCAATTA 300
QY 7288 tatggtcagctactcttttagtaaaatacttttggatagcgttggacagataagatctat 7347
|||||
Db 301 TATGTCAGTCTACTTTTAGTAGAATTTTGGATAGCGTTGACACGATAGATCTTAT 360
QY 7348 tccatactcttacttaattgaataatttatttcaatttttgccttcaattatlaacata 7407
|||||
Db 361 TCCATACCTCTTAATTTATGATTAATTTATTTATTTATTTTCTTCAATTATTAACATA 420
QY 7408 ttltgtgtggaagaaggttggccttttttgaagaagcaaaattatataacacataa 7467
|||||
Db 421 TTTTGTGTGGAAGAGGTTGGCTTTTGTGAAGACAAATTAATTAACCACTAA 480
QY 7468 cactccttttggacataaagccttattcattcattcctcgaagataataataattt 7527
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Db 481 CACTCTCTTTTGAATATTAAGCCTTATTCATCTCGAAGATATTTTATAAATTT 540
QY 7528 attttttaaattgaattctcgaattattatcttaaatattgattttaaagagacta 7587
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Db 541 AATTTTAAATTAAGATTTTCGAATTAATTTATCTTAATTAATTTTAAACGACATA 600
QY 7588 ttatgtgaagaaactttttatagaagaattcaagaagatttgaatttgcctt 7647
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Db 601 TTATGTCAGCAACTTTTAAATGAGCAATTTGATGATGATTAAGAAATTTTCTCTCT 660

QY 7648 gaaagaagcttccctgtgataagaaatgatg 7678
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Db 661 GGAAAGAGCTTTCCTTCAGTGAATATGATG 691

RESULT 9

LOCUS

AUI17220

DEFINITION

AUI17220

ACCESSION

AUI17220

VERSION

AUI17220.1

KEYWORDS

PST

SOURCE

Human

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 742)

AUTHORS

Ohtsuki, Nishikawa, Y., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,

Yamamoto, Y., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and

Isogai, T.

JOURNAL

Unpublished (2000)

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1512-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81 438-52-3951

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Email: genomics@hri.co.jp

HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

FEATURES

Location/Qualifiers

1..742

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="HEMBA1009116"

/clone_lib="HEMBA1"

/tissue_type="whole embryo, mainly head"

/dev_stage="embryo, 10 weeks"

/note="Vector: pME185FL3"

BASE COUNT 249 a 183 c 161 g 164 t 5 others
ORIGIN

Query Match 6.4%; Score 656.6; DB 9; length 742;
Best Local Similarity 98.2%; Pred. No. 7.1e-90;
Matches 714; Conservative 0; Mismatches 8; Indels 5; Gaps 5;

QY 3386 atgcacagtgatgacatc-agaagcttcaactgacatccagacellaaacatca 3444
|||||
Db 1 ATCCAAAGCGTCTGACCTTACCAAGACCTTACCTGACCTGACCTTAAACATCA 60
QY 3445 ttaacaaacaacagtgtagacatatatagagagagacagaagaagccttaacccag 3504
|||||
Db 61 TTAAACAAACAGCGTAGCAGTATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 3505 aagacatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 3564
|||||
Db 121 AGGACCTTCAGGCTGAGCAGCTCAACAAACACACAGGCGCCAGCAATGAGAGCA 180
QY 3565 atagaagccgctttagaagagatcagaagatcactlaactgaagatccagagagaa 3624
|||||
Db 181 ATGGAAGCCGCTTGAAGAGAGCTGAGAGAGATCATTAAGTCAAGCAGAGAGAA 240
QY 3625 ttccatctccagcctgaatgaatgaagagccagagtgatgactgaagagcattctg 3684
|||||
Db 241 TTCACTCCGAGGCTAAGTAATAGAGAGCCAGGAGGCTATTGACTTAAAGCATCTCG 300
QY 3685 ctcaagagcagtcagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3744
|||||

Db 301 CTCACGACCCAGCTCTGGTACGCCAAACTCTGGATATTCACAAAGATGCAACCTTTGC 360
 QY 3745 acatcagataaagaagtcctcaggaagactgagatccaggaataagttatccsfat 3804
 Db 361 ACATTCCATATAAAGTCTCCAGGAAGTACTGAGATCCAGAAATAGTTATCCGTAT 420
 QY 3805 ctgaagggaagaagtcctgagagagcaagtcctatagaagaatcatgagactgcga 3864
 Db 421 CTGAAGGGAAGAGTCTGAGAGAGCAGTCTATAGAAAAGTACATGAGACCTGGGA 480
 QY 3865 aaccacccaattatccaccacagagacccatattgaaaagatccagatccacttttg 3924
 Db 481 AACACCCAAATATTCACACACAGCACCCTATTTGAAACAGTACACGATACCCACTTTTG 540
 QY 3925 gacttcccttgatcagatcagactccagagtgagatga-cttgagctgagcttcagat 3983
 Db 541 GNCCTTCCCTTTGT-CATATGACTTCCAGAGTGAANTGATTTGGCTGGGTTCTGGAGGT 599
 QY 3984 aaatat-aagcttccgttccctggaatccgcaactcttgagtcagctgagctgcacc 4042
 Db 600 AAATATAAGCTCTCCGTTCTGGGAAATCCGCACTACTTGAGTCAGTGCCCTGGGCTAC 659
 QY 4043 aaatcttgcacaaactatgctcctatcccaacttc-aatctgctcctcaattttcag 4101
 Db 660 AAATCTTCCCAAACTATGTCCTTATCTCCACTTCAATCAATCTGCTCTCANTTTCAA 719
 QY 4102 ctgttgg 4108
 Db 720 CTGTTTG 726

RESULT 10
 LOCUS B1686434 886 bp mRNA linear EST 18-SEP-2001
 DEFINITION 603312804F1 NCI_GCAP_Mam6 Mus musculus CDNA IMAGE:5552984 5',
 accession B1686434
 VERSION B1686434.1 GI:15649062
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 TITLE NIH-MGC http://mgc.nci.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 EMAIL: cgapbs-tr@mail.nih.gov

CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 CDNA Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM11897 row: 9 column: 01
 High quality sequence stop: 772.

FEATURES

Location/Qualifiers
 1..886

/organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:5552984"
 /clone_1lb="NCI_GCAP_Mam6"
 /sex="female, virgin"
 /tissue="type:infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt:
 Site 2; Noli; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 268 a 248 c 189 g 181 t
 ORIGIN

Query Match 6.3%; Score 652.8; DB 10; Length 886;
 Best Local Similarity 90.1%; Pred. No. 2.5e-89;
 Matches 744; Conservative 0; Mismatches 77; Indels 5; Gaps 4;

QY 3310 gctccgagtgcttctgtcccaattgctcagacacaaagacactctctcggcaagaatg 3369
 Db 25 GATCTGATGTTTGTGTGCCAATTTGCTGACCAAAAGACCTCTCTGCAAAAGATG 84
 QY 3370 caaatgggagatgatagtatgaagtgctgctcctacccgaagcttcactgactcca 3429
 Db 85 CAATGGGGATATGATGATGCAATGATGATGATGATGATGATGATGATGATGATGATG 144
 QY 3430 ggcctttaaacaatcaaaacaaacagtgagcagatattatgaaggaagaaagaa 3489
 Db 145 GGCCTTTAAATCATATTTAAACAAACACAGCGAGCATTTATTAAGACGACAAAGAA 204
 QY 3490 agcgccttaaccagagagcacttcagctcagcagcctcaacaacagcagagagca 3549
 Db 205 AGCGCTTAACCCAGAGGCACTTCAAGCTGAGCAGCTCAACAAACAGAGGGAATG 264
 QY 3550 atgagagagcaagtcataatgaagccgcttagagagagagtcagaagatcctaac- 3608
 Db 265 GGGAGAGCAGCTCAATGAGAGCCCTTTAGAGAGAGGTGAGAGATCACTTAACGTAA 324
 QY 3609 agtcacagagagaatccactccacagccttaagtaataatagaagcccaaggttcattg 3668
 Db 325 AGTCATCCGAGAGAAATTTCCACTTCCAGCTGAGTAAATACCAACCCAGGATTCATTG 384
 QY 3669 actaaagacatctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 3728
 Db 385 ACTAAAGCCATCTGCTCAGAGCCACTCTGCTGAGCAGCACTTGATATTCACAAA 444
 QY 3729 aggtatgaaccttgcacatcagataaagaagtcctcaggaagagtcagatccagga 3788
 Db 445 AGGATGCAAGCTTTGCAATTCAGATTAAGTCTCAGAAAGTACAGAGATCCAGGA 504
 QY 3789 aatagttatcagtcagtaagaagaa-aggaaagttcaggaagcagtcctcctataga 3847
 Db 505 AATAGTTATTCATCCGTATCTATCTATGAGAACAGAAAGTTCTGAAAGAGGACCCCATTCGAAAA 564
 QY 3848 gtacatgaagacctcagaaacacccaattatccaccacagcagcagcagcagcagcagc 3907
 Db 565 GTACATGAGACCTGCAAAACCCCAACTATTCTCCACAGGAGAGCCATCGAAAAA 624
 QY 3908 ccagttaccacatttggagcttcccttgatcataatgagcttcagagtgagtgatg 3967
 Db 625 CCATACCCCGCTTTGGAGTACCTTATGATACATTAATGATCTCCAGAGTGAAGCTGATG 684
 QY 3968 gctgagcttgagtaataaagcctcagctcagctcagcagcagcagcagcagcagcagc 4026
 Db 685 GCTACGGTTTGGAGTAATATTAAGCTCTCGGTTCTCGGAAATCGGCACTCTGGAAGCTC 744
 QY 4027 acgtgctgagcctaccacatcccttgcaaaacatgctcctacccacactcaatctgc 4086
 Db 745 ATGTCCTGCTTACCAAAATCTTGCACAAACCTATGAGCTTATTCACACATCAACCTGC 804
 QY 4087 ctccatcttttcagctg-cttgatcagaagaatgacatcctcta 4130
 Db 805 CTCCTCATTTCCAGACGACGACGATCAGACAAATCAATCAATCCCTCA 850

RESULT 11
 LOCUS BF982937 1043 bp mRNA linear EST 23-JAN-2001
 DEFINITION 602306330F1 NIH_MGC_88 Homo sapiens CDNA clone IMAGE:4397719 5',
 accession BF982937
 KEYWORDS BF982937.1 GI:12385749
 EST.

SOURCE
ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1043)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Invitrogen, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LLM10098 Row: 1 Column: 08
High quality sequence stop: 642.
Location/Qualifiers
1..1043
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="4397719"
/clone_lib="NIH-MGC-88"
/issue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site:1: NCI; Site:2: Sall; Cloned unidirectionally;
Oligo-dr primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH-MGC library."
BASE COUNT 317 a 260 c 293 g 173 t
ORIGIN

Query Match 6.3%; Score 649.2; DB 10; Length 1043;
Best Local Similarity 95.1%; Pred. No. 8.3e-89;
Matches 702; Conservative 0; Mismatches 33; Indels 3; Gaps 3;

QY 3022 gaggggagagacatctctgaggggagtcctgcataacccaagaagcctgggagctga 3081
DB 11 GAGGGGAGACATCTCTGGGGGAGTCCGTCATACACCAAGCCTGGGGCTGCTGA 70
QY 3082 cgcctgtctgcagcccaagagagagac-aaagactcaagagatgctcccaatggag 3140
DB 71 CGCCTGTCTGGACACCAAGAGAGAGAAAGACTCTAAGGAGATGCCAATGTGGAG 130
QY 3141 gccgcccacatcggcgagacattatgtgcttggctgtgaaacaaagagattcctgcag 3200
DB 131 GCCAGCCATCTGGCGCGAGATATTATGCTTGGCTGGAACCAAGCGATTCCTGCAG 190
QY 3201 gggggcgagcgtggcgagaaatctcgggggcccctcccagcagatctcgtacatcgga 3260
DB 191 GGGGGCGAGCTGGGAGAGAAAGTCTGGGGCCCTCCCAACAGTATCTGCATGGGGA 250
QY 3261 gaaacaaagtcacaaagtaatcccaagtcctcgttaccagagagcgtacagctcgtgtt 3320
DB 251 GAAACAAAGTCCAAAGATGATCCAGTCCCTGTACAGAGCCGTAAGAGCTCCGTTT 310
QY 3321 ttlttgccaattgcctgcagcaacaaagacccctcctcgtgcgaagaatgcgaatggcga 3380
DB 311 TTTTGTGCCAATTGCTGACCAACAAAGACCTCTCTGCGGAAGAAATGCAAAATGGCGGA 370
QY 3381 tatgtatgaagcgtgtgagcctctacagaagcttaccatctgactcccaagccttaaac 3440
DB 371 TATGTATGCAAGCGCTGTGGCTCTTACCAAGCTTCACTGACTCCCAAGCCTTTAAC 430
QY 3441 atcattaaacaaacaaacagtgtagcagattatgagagagagaaacaaagcgcctaac 3500
DB 431 ATCATTAACAAACAAACAGCGTAGAGAGATTTATAGAGAGAGAAAGAAAGCCCTTAAC 490
QY 3501 cgaagagcacttcagagcgtcgaacaaacagcagagggcagcaatgaagagca 3560
ORIGIN

DB 491 CCAGAGGACTTCAAGCTGTAGACGCTCAACAAAGAGAGGGGCGCATATGAGAGCA 550
QY 3561 gtaactgaagcccgcttagagagagagtcagaagatcatctaaatgacagaga 3620
DB 551 GTCAATGAAGACCCGTTAGAGAGAGGCTCAAGAAATCATCTAAGTAAAGTACCAGGA 610
QY 3621 gaattcactccacagccttaaglaatacgaagcccaaggtt-cattgaactaaagcca 3679
DB 611 GAATTTGA-TCCCAAGACTAAGTAATATGCAAGCCAGGCTTCATTGAGTAAAGGCA 669
QY 3680 ttctgtcagagcagcagctcgtgtaagccaacitcgtatcacaagaagagca 3739
DB 670 TTCTGTGTAGAGGACGACTCTGTTCAGCAAAACTGTGGATTTCACAAAGGTTGACCC 729
QY 3740 ttgacatcagataa 3757
DB 730 TTGGCCCTTAGATACAA 747

RESULT 12
BI492548 649 bp mRNA linear EST 28-AUG-2001
LOCUS DE25107.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
DEFINITION IMAGE:2484612.3', mRNA sequence.
ACCESSION BI492548
VERSION BI492548.1 GI:15331892
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R.
and Morton,C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA
library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
95130111
Contact: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and
Reproductive Biology
B-1gham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
Email: cmorton@bics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes
of Health Intramural Sequencing Center (NISC; see
<http://www.nisc.nih.gov>).
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LLM6182 Row: K Column: 13
Seq primer: 5' primer.
Location/Qualifiers
1..649
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2484612"
/clone_lib="Morton Fetal Cochlea"
/issue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ear; Vector: Bluescript SK-; Site:1: EcoRI;
Site:2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
unidirectionally. Primer: Oligo dr. fetal cochlea, normal.
37% of inserts 0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-TAP
XR Vector. Library constructed by N. Robertson, C. Morton.
-5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor
sequence: 5' CTCGACTTTTCTTTTCTTTT 3'."
BASE COUNT 217 a 131 c 97 g 204 t
ORIGIN

A0117175 649 bp mRNA linear EST 19-OCT-2000
 LOCUS A0117175 HEMBA1 Homo sapiens cDNA clone HEMBA1000822 5', mRNA
 DEFINITION
 ACCESSION A0117175
 VERSION A0117175.1 GI:10932121
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 649)
 AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
 Isogai, T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3951
 Fax: 81-438-52-3952
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
 Location/Qualifiers
 1..649
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1000822"
 /clone_1lb="HEMBA1"
 /issue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: pME18SFl3"
 BASE COUNT 207 a 109 c 121 g 209 t 3 others
 ORIGIN

FEATURES
 source 1..649
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HEMBA1000822"
 /clone_1lb="HEMBA1"
 /issue_type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: pME18SFl3"
 BASE COUNT 207 a 109 c 121 g 209 t 3 others
 ORIGIN
 Query Match 6.1%; Score 630; DB 9; Length 649;
 Best Local Similarity 99.5%; Pred. No. 7.9e-86;
 Matches 641; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5306 gatgaaccagatgattgcttcttaagcctcctggtgttactaactctactgca 5365
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 Db 1 GATGAACCAAGATGATGATTTCTTTTGAAGCTCTCTGTTGTTACTTAATCTCACTTGCA 60
 QY 5366 catataactaaaggaatccctcaattcaaaagcatagatgatacaaatgtcagaccg 5425
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 CATATTAACCTAAAGGAATCCCTCAATTCMAAGCATAGATGATCAATATCTCAGACCG 120
 QY 5426 tgggttaattgttagaacaatgagcatttcttcaacaagtaacctgctattatt 5485
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 TGGCTTTAATTTGTTTGAACACATGGCATTTCTTCAACAGGTAACCTCTCTATTATT 180
 QY 5486 tatlltcllttggtlaataatltccaacttltgtcagcagcgctcaaggtttac 5545
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 TATTTCTTTTGGTTAAATATATTTCCAACTTTTGTCAGCGACGCTTAAAGTTTAC 240
 QY 5546 gttaaccaagactgcaagttgttatatgtaccagcaatccctcattaaatgtatcacg 5605
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GTTACCAAGACTGACAGTTGGTATATGTACACCAATCCCTTCAATTAATATGATACAG 300
 QY 5606 attagtaagtagcattaaatagagattcttagaagaatgtctctctatagaactttaata 5665
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 AATTATGTTAACTACATTAATATGATGATTTTGAAGATATGCTCTCATTAACAATTTTAAATA 360
 QY 5666 cttaagacttctgttaaaaactatccatgaagaggaagctcctcagcattacgcctcagga 5725
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 CTTAAGCTTTTGTATAAACTATTCATCATGAAGGAAGAGCTCTCTCAGCATTAATCTCTCAGGCA 420

QY 5726 aataggcctaactgaactgaactaaatgaattgttgaagggcgctgttagctgagcctca 5785
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 AATAGGGCTAAATTAACCTGAACATTAATTAATTTGTTAAAGGTGCTGTAGTCAAGCTCA 480
 QY 5786 atgttctcaagaagatgaatgaactgaactgaactgaactgaactgaactgaactgaactgaact 5845
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 Db 481 ATGCTTCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 5846 caaccagtagattatatttttgcacagagatgtagaagatlatcaagaactactgagca 5905
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 Db 541 CAACAGTAGATTATTTTGGCAGGAGATGTANAGATATTAACACTCTGTGATGCA 600
 QY 5906 ct-gtcagattactatttcaatgaagaagttggagagaaca 5948
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 Db 601 CTGTCAGATTAACTATTTCATTAAAGAGTTGGAGAACAA 644

RESULT 15
 LOCUS BG779571 679 bp mRNA linear EST 15-MAY-2001
 DEFINITION BG779571 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:480793 5',
 mRNA sequence.
 ACCESSION BG779571
 VERSION BG779571.1 GI:14049888
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 679)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: c9qab@femail.nih.gov
 Tissue procurement: DCTD/DP
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNI)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNI at:
<http://image.lmni.gov>
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 High quality sequence stop: 679.
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 /clone_1lb="NIH_MGC_60"
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 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: prostate; Vector: PDNR-LIB (Clontech);
 Site 1: SfiI (ggcgctggcc); Site 2: SfiI (ggcgataggcc)
 5' and 3' adaptor cDNA was prepared from cell line RNA.
 adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor
 sequence: 5'-ATTCTAGAGCCGAGCGCCAGCATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 library."

FEATURES
 source 1..679
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH-MGC
 library."

BASE COUNT 224 a 107 c 129 g 218 t 1 others
 ORIGIN

Query Match 6.1%; Score 629.4; DB 10; Length 679;
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 Matches 674; Conservative 0; Mismatches 2; Indels 4; Gaps 4;
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 21, 2002, 16:51:33 ; Search time 11495.2 Seconds

(without alignments)
19413.717 Million cell updates/sec

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Scoring table:
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Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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30	1186.2	11.5	1205	26	US-09-668-179-156
31	1186.2	11.5	1205	55	US-60-168-432-279

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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32 1136.2 11.0 37066 63 US-60-243-468-190 Sequence 190, App
33 1060.4 10.3 10662 37 US-10-029-386-25248 Sequence 25248, A
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35 1007 9.8 1009 23 US-09-602-877-107 Sequence 107, App
36 1007 9.8 1009 23 US-09-602-877A-107 Sequence 107, App
37 1007 9.8 1009 27 US-09-687-507-107 Sequence 107, App
38 1007 9.8 1009 27 US-09-687-507A-107 Sequence 107, App
39 1007 9.8 1009 30 US-09-778-381-107 Sequence 107, App
40 864.6 8.4 1038 29 US-09-758-469-134 Sequence 134, App
41 852.8 8.3 965 25 US-09-652-355-9624 Sequence 9624, App
42 852.8 8.3 965 25 US-09-652-814-8751 Sequence 8751, App
43 761.4 7.4 766 18 US-09-417-031-11 Sequence 11, App1
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45 717 7.0 717 25 US-09-652-127-8850 Sequence 8850, App

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ALIGNMENTS

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/ Sequence 1, Application US/09702216
/ GENRML INFORMATION:
/ APPLICANT: Gish, Kurt C.
/ APPLICANT: Mack, David.
/ TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING BREAST CANCER,
/ TITLE OF INVENTION: COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST
/ FILE REFERENCE: A-69026/DJH/JJP
/ CURRENT APPLICATION NUMBER: US/09/702, 216
/ PRIOR APPLICATION NUMBER: US 09/525, 361
/ PRIOR FILING DATE: 2000-03-15
/ PRIOR APPLICATION NUMBER: US 09/453, 137
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: US 09/450, 810
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US 00/06952
/ PRIOR FILING DATE: 2000-03-15
/ NUMBER OF SEQ ID NOS: 3
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 10315
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (10118)..(10180)
/ OTHER INFORMATION: "n" at positions 10118 and 10180 can be any base.
US-09-702-216-1

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Best local similarity 100.0%; Pred. NO. 0;
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; Sequence 20, Application PC/TUS0032056
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Calferkey, Robert
; APPLICANT: Recipon, Hervé
; APPLICANT: Sun, Yongming
; APPLICANT: diadexus, Inc.
; TITLE OF INVENTION: A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING,
; FILE REFERENCE: IMAGING AND TREATING BREAST CANCER
; CURRENT APPLICATION NUMBER: PCT/US00/32056
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 60/166,973
; PRIOR FILING DATE: 1999-11-23
; NUMBER OF SEQ ID NOS: 21
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Query Match          96.5%; Score 9951; DB 1; Length 10006;
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? GENERAL INFORMATION:
? APPLICANT: Salceda, Susana
? APPLICANT: Caferkey, Robert
? APPLICANT: Recipon, Hervé
? APPLICANT: Sun, Yongming
? TITLE OF INVENTION: A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING
? TITLE OF INVENTION: IMAGING AND TREATING BREAST CANCER
? FILE REFERENCE: DEX-0117
? CURRENT APPLICATION NUMBER: US/09/721,183
? CURRENT FILING DATE: 2000-11-22
? PRIOR APPLICATION NUMBER: 60/166,973
? PRIOR FILING DATE: 1999-11-23
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RESULT 7
PCF-US01-01334-6816/c
Sequence 6816, Application PCF/TUS0101334
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc., et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC010PCT
CURRENT APPLICATION NUMBER: PCF/TUS01/01334
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/226,868
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PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/225,267
PRIOR FILING DATE: 2000-08-14
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PRIOR FILING DATE: 2000-07-07
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PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
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PRIOR FILING DATE: 2000-08-14
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PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/241,809
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/249,299
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PRIOR APPLICATION NUMBER: 60/236,327
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PRIOR APPLICATION NUMBER: 60/241,785
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/244,617
PRIOR FILING DATE: 2000-11-01

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25	PRIOR FILING DATE: 2000-11-17	
26	PRIOR APPLICATION NUMBER: 60/232, 400	
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28	PRIOR APPLICATION NUMBER: 60/231, 242	
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61	PRIOR FILING DATE: 2000-09-14	
62	PRIOR APPLICATION NUMBER: 60/232, 398	

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2840 ATCTCGAAGATATTAATTAATTAATTTATTTTAAATTAAGATTTCTGAATTAATTA 2781
7562 cttaaatlgtatlltaaacgaactaltatgttagagaactlltttaalagaagaattc 7621
2780 CTTAATTTGATTTTAAACGACCTATTATGCTAGCGAATCTTTTAAATGAAGAAATTC 2721
7622 atgaagatttgaagatttctccttcttgaagaagcttccctgtatgaataatgtatgc 7681
2720 ATGATGATTTAGAAATTTCTCTTGGAAAGGCTTCCCTGATGAAGAAATGATGAGC 2661
7682 cagctaaatgtgtgtgcatatttaaaactgaaatatttaaaattatgttctatctc 7741
2660 CAGCTAAATTTGTGCGCATTTTAAACGAAATTAATTTTAAATTAATTTGCTATATTC 2601
7742 taaattgagctllgatacaactlltagcagaggaagcactltagctllctatllctt 7801
2600 TAAATTTGAGCTTTGATCAACCTTTAGCCAGAGCAAGCACTGATGCTGCTCATTTCTCT 2541
7802 ttttcaactcttctcactcaactcaactcgtatctatcttcttcttcttcttcttctt 7861
2540 TTTTCACTCTTCTCTCATCACTCACTCTGATATCTTCTGTTGTTGGATGAGAAA 2481
QY 7862 atcataagagcaaacatcctcaagaagttgtgtatttggagagcactacaatgctcc 7921
|||||

Dh 2480 ATCATAAAGACCAACCCACTCTCAGAACGTTCTGATTTGAGAGACACTACATGACTCC 2421
Qy 7922 aagfatafagaagaagagagagctcaatfaglaactctctgtaagttcaaaagaaag 7981
Dh 2420 AAGTATATGAGAAAGAGAGAGAGCTTAATGATTAACCTGTAGTGAAGAGAGAGAG 2361
Qy 7982 tatgccaattctctctacatgacatactagaatttttttaataaactttaagatg 8041
Dh 2360 TATGCCCAATTCCTCTCMATGACATATGAGTTTTTTTATATCAACTTTTAAAGTAGT 2301
Qy 8042 galgctctgctcctaaactgctctgctttagtgaagtagatctttataaacaagatg 8101
Dh 2300 GATGCTCTGCTTAAACTGTTCTTTTACTGAGGTAAATTTTATATAAACAAGCATGG 2241
Qy 8102 ggaattctttctaaagtaatactaaatgaagaaggaagaaatgtaactttaacagctcttg 8161
Dh 2240 GGAATCTTTCTTAAGGTATATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2181
Qy 8162 ttgaagccctgctgtagcacatctatgtaataatgtaactgtaactgtaactgtaactg 8221
Dh 2180 TTGAAGCCCTGCTGAGCATATATGATTTATATGATGACATGTCATTAATATATATGA 2121
Qy 8222 tccaatgcaaatagagctccaaataatataatgtaataatataatataatataatgta 8281
Dh 2120 TCCAAATGCAAAATACAGCTCCAAAATATTAATATATATATATATATATATATATAT 2061
Qy 8282 aatacaatttcttaataactgaagaagctgaatagagctgaatataataatataatagcc 8341
Dh 2060 AATACATTTTTTTTATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2001
Qy 8342 tccctgctgctgtagcgaacacacacaaagtgagagctctgagagctctgagagctg 8401
Dh 2000 TCTGTGTTGCTGCTGCAAAAACATCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1941
Qy 8402 cccctgctttagttaaataatgcaattctcagaaggggaatactctgacatccagtggt 8461
Dh 1940 CCGCTGTTTACTTAATATTAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1881
Qy 8462 ggaatgtagaggaagaaagagctgtagctgctgctgctgctgctgctgctgctgctg 8521
Dh 1880 GGAATGCTGAGCTTAAG 1821
Qy 8522 taagttgag 8581
Dh 1820 TAACTGAG 1761
Qy 8582 aaaaagaagaaag 8641
Dh 1760 AAAAAAG 1701
Qy 8642 gtccaaag 8701
Dh 1700 GTCCAAAGGAG 1641
Qy 8702 tctaaatcaaaagtagtagcttaggctgaatctcagagagagagagagagagagagag 8761
Dh 1640 TCTAATCAAAAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 1581
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Dh 1580 GAAGATAG 1521
Qy 8822 ggcgaag 8881
Dh 1520 GGCAG 1461
Qy 8882 ttcatag 8941
Dh 1460 TTCAATAG 1401
Qy 8942 gtaattgag 9001
Dh 1400 GTTAATGCTTAATGAG 1341

Qy 9002 acatgaagaagatgtaaatctcaagatcaatccacagtggaagaactagacatgacat 9061
Dh 1340 ACATGAG 1281
Qy 9062 tcatgcttctctggaaggaag 9121
Dh 1280 TCATGCTGCTCTTGAAG 1221
Qy 9122 aaaagcagaag 9181
Dh 1220 AAAAGCAG 1161
Qy 9182 tcttag 9241
Dh 1160 TTCTAG 1101
Qy 9242 tttcccaacataag 9301
Dh 1100 TTTTCCCAACATATGAG 1041
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Dh 1040 CTGTAATAATTTGAAAAAT 981
Qy 9362 tactgtttagtaag 9421
Dh 980 TACTGTGTTGTAAG 921
Qy 9422 ttattatgag 9481
Dh 920 TTATATATGAG 861
Qy 9482 gttcatlcttcttaagaag 9541
Dh 860 GGTTCATTTTTTTTAAAG 801
Qy 9542 gaagatgcaaaactatctagagctgaataacatagcttcttaagtgctacacaaag 9601
Dh 800 GAAGATGCAAAACTATCTAG 741
Qy 9602 gcaaatatacaaatataaag 9661
Dh 740 GCAAAATATCAAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 681
Qy 9662 aaaaacttggag 9721
Dh 680 AAAACTTTGGGAG 621
Qy 9722 acagaataatccag 9781
Dh 620 ACAGCAATATTCAG 561
Qy 9782 aagaatccaattgtagctgag 9841
Dh 560 AAGAAATTCATTTGATCTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 501
Qy 9842 cttaacacacag 9901
Dh 500 CTTACACACAG 441
Qy 9902 tctactcaaaacatgctctgtagtattctctatgcaaaacatctcagagagagagagagag 9961
Dh 440 TCTACTCAAAACATGCTCTGGGTATTTCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 381
Qy 9962 tgcctgtctacatcaaatggaataaagtttccacacagttacacaaagagagagagagag 10021
Dh 380 TGTCTGTATCAATCAAAATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 321
Qy 10022 gtaatggttataag 10081
Dh 320 GGTATGCTTTATATGAG 263

1 PRIOR APPLICATION NUMBER: 60/225,213
2 PRIOR FILING DATE: 2000-08-14
3 PRIOR APPLICATION NUMBER: 60/227,182
4 PRIOR FILING DATE: 2000-08-22
5 PRIOR APPLICATION NUMBER: 60/225,214
6 PRIOR FILING DATE: 2000-08-14
7 PRIOR APPLICATION NUMBER: 60/235,836
8 PRIOR FILING DATE: 2000-09-27
9 PRIOR APPLICATION NUMBER: 60/230,438
10 PRIOR FILING DATE: 2000-09-06
11 PRIOR APPLICATION NUMBER: 60/215,135
12 PRIOR FILING DATE: 2000-06-30
13 PRIOR APPLICATION NUMBER: 60/225,266
14 PRIOR FILING DATE: 2000-08-14
15 PRIOR APPLICATION NUMBER: 60/249,218
16 PRIOR FILING DATE: 2000-11-17
17 PRIOR APPLICATION NUMBER: 60/249,208
18 PRIOR FILING DATE: 2000-11-17
19 PRIOR APPLICATION NUMBER: 60/249,213
20 PRIOR FILING DATE: 2000-11-17
21 PRIOR APPLICATION NUMBER: 60/249,212
22 PRIOR FILING DATE: 2000-11-17
23 PRIOR APPLICATION NUMBER: 60/249,207
24 PRIOR FILING DATE: 2000-11-17
25 PRIOR APPLICATION NUMBER: 60/249,245
26 PRIOR FILING DATE: 2000-11-17
27 PRIOR APPLICATION NUMBER: 60/249,244
28 PRIOR FILING DATE: 2000-11-17
29 PRIOR APPLICATION NUMBER: 60/249,217
30 PRIOR FILING DATE: 2000-11-17
31 PRIOR APPLICATION NUMBER: 60/249,211
32 PRIOR FILING DATE: 2000-11-17
33 PRIOR APPLICATION NUMBER: 60/249,215
34 PRIOR FILING DATE: 2000-11-17
35 PRIOR APPLICATION NUMBER: 60/249,264
36 PRIOR FILING DATE: 2000-11-17
37 PRIOR APPLICATION NUMBER: 60/249,214
38 PRIOR FILING DATE: 2000-11-17
39 PRIOR APPLICATION NUMBER: 60/249,297
40 PRIOR FILING DATE: 2000-11-17
41 PRIOR APPLICATION NUMBER: 60/232,400
42 PRIOR FILING DATE: 2000-09-14
43 PRIOR APPLICATION NUMBER: 60/231,242
44 PRIOR FILING DATE: 2000-09-08
45 PRIOR APPLICATION NUMBER: 60/232,081
46 PRIOR FILING DATE: 2000-09-08
47 PRIOR APPLICATION NUMBER: 60/232,080
48 PRIOR FILING DATE: 2000-09-08
49 PRIOR APPLICATION NUMBER: 60/231,414
50 PRIOR FILING DATE: 2000-09-08
51 PRIOR APPLICATION NUMBER: 60/231,244
52 PRIOR FILING DATE: 2000-09-08
53 PRIOR APPLICATION NUMBER: 60/233,064
54 PRIOR FILING DATE: 2000-09-14
55 PRIOR APPLICATION NUMBER: 60/233,063
56 PRIOR FILING DATE: 2000-09-14
57 PRIOR APPLICATION NUMBER: 60/232,397
58 PRIOR FILING DATE: 2000-09-14
59 PRIOR APPLICATION NUMBER: 60/232,399
60 PRIOR FILING DATE: 2000-09-14
61 PRIOR APPLICATION NUMBER: 60/232,401
62 PRIOR FILING DATE: 2000-09-14
63 PRIOR APPLICATION NUMBER: 60/241,808
64 PRIOR FILING DATE: 2000-10-20
65 PRIOR APPLICATION NUMBER: 60/241,826
66 PRIOR FILING DATE: 2000-10-20
67 PRIOR APPLICATION NUMBER: 60/241,786
68 PRIOR FILING DATE: 2000-10-20
69 PRIOR APPLICATION NUMBER: 60/241,221
70 PRIOR FILING DATE: 2000-10-20
71 PRIOR APPLICATION NUMBER: 60/246,475
72 PRIOR FILING DATE: 2000-11-08
73 PRIOR APPLICATION NUMBER: 60/231,243

1 PRIOR FILING DATE: 2000-09-08
2 PRIOR APPLICATION NUMBER: 60/233,065
3 PRIOR FILING DATE: 2000-09-14
4 PRIOR APPLICATION NUMBER: 60/232,398

Query Match 65.7%; Score 6774.6; DB 30; Length 10246;

Best Local Similarity 99.0%; Pred. No. 0;

Matches 6859; Conservative 0; Mismatches 26; Indels 40; Gaps 3;

1 3422 gaccccaagcccttaacatcatlaaacaacaacggtgagcagatattagagagag 3481
2 6920 GACCCCAAGCCCTTAAATCATTTAAACAAAACAGGCTGACAGATTTATAGAGAG 6861
3 3482 aacaagaagcgcccttaacccagagagccttcaggtgcagcctcaacaacagcagag 3541
4 6860 AACAAAGAAAGCGCCTTAACCCAGAGGCACTTCAAGGCTGAGCAGCTCAACAAAGCAGAG 6801
5 3542 ggggaagaatggagagcagatcaatgaaagccggttagagagaggttagaagatcatc 3601
6 6800 GGGGAGCAATGAGAGCAAGTCAATGGAACCCGTTAGAGAGAGCTCAGAACATCATCT 6741
7 3602 aactgaagtcacccagagagaatcccaatcccaagccctaaatlaagagcccaagg 3661
8 6740 AACTGAAAGTCACACAGAGAGAAATTCACCTCCACCTTAATTAATGAAAGCCAGG 6681
9 3662 tcaatgactaaagacatctcgtcagcagcagtcctcgtgcagcacaactcgtat 3721
10 6680 TTCAATTACTAAAGCACTCTGCTCAGCAGCAGCTGCTGTCACCCAACTTGGATAT 6621
11 3722 tcbaaagaagatgcaactcttcagcatcagaataaagctcccaagaagatcagaga 3781
12 6620 TCAAAAAGGATGCAACCTTTGACATTCAGATTAATAATCTCCAGGAAATCTGAGAA 6561
13 3782 lccaggaatagltacccgtatcgtatcgaaggaagaaagttctgagaagcgatctat 3841
14 6560 TCCAGGAATAGTTCATCCGATATCTGAAGGAAAGAAATTTGAGAGAGCCAGCTCTAT 6501
15 3842 agaaagatcatgagacctcgcgaacaacccaatlaattcaccacagcagccctatga 3901
16 6500 AGAAAAGTACATGAGACCTGCGAACAACCCCAATTTTCACCAAGCAGGACCTTTGA 6441
17 3902 aaagttccagttcccaacttttggactcccttgcataatgaactccaagatgaagc 3961
18 6440 AAAGTCCAGTACCCCACTTTTGGACTTCCTTTGACATAAATGATTCAGAGCTGAG 6381
19 3962 tgaatgctgcggtcttgagtaataataagctccgtctcgttggaatccgcactat 4021
20 6380 TGATGGCTGCGGTTCTGGAGTAAATATAGCTCTCCGTTCTGGAAATCCGACTACTT 6321
21 4022 gagtcagctgctgcgtcctcaaatccctgcgaactatgctcctatcccaactcaaa 4081
22 6320 GAGTCAGCTGCTGCGCTACCAATCTTCCMAAATGATGCTTATCCCACTTCA 6261
23 4082 tctgcctcctcaatttttagctgttgatcagaatgaactcctctagatttggcat 4141
24 6260 TCTGCTCCCTCAATTTTACGCTGTGGATCAGCAATGACATTCCTCTAATTTGGCAT 6201
25 4142 caagcaltccagacctgggccaactgcaacggtgctcccaagagagaacgaagcacc 4201
26 6200 CAAGCAATCCAGACCTGGGCCAATGCAAAAGCTGCTTCAAGAGGAAAGCAAGCAC 6141
27 4202 accaaatgtaaaaaatagaaggtcccttgaatgagtaaaaaacagagaagttagaag 4261
28 6140 ACCAAATGTAAAAATGAAGGTCCCTTGAATGTATTAATAACAGAAAGTATGTAAG 6081
29 4262 tactcaagaatgaacttcaaaaaatgtgtgcaactgtggcatgtcttcttgatgaagt 4321
30 6080 TACTCAAGATGACCTTTAAACAAATGTGTGCACTGTGGCATGTCTTTTGATTAAGT 6021
31 4322 gatgtatgcttgcatatgaatgcaatgcaatgcaatgcaatgcaatgcaatgcaatg 4381
32 6020 GATGTATGCTTTGATATGATGATGATGATGATGATGATGATGATGATGATGATG 5961

QY	4382	caagatccttttgacagacaaatctgtcttcaacaacalctcagagggccgtgcatag	4444
Dp	5560	ccagagcttttgacacgcaaaatgtgactttccaaacacatmttccacagagccctgcataag	5501
QY	4442	gaacatgcacagctggaaaanaaattgaanaccctaaagtaagtaaaccttaacattagca	4501
Dp	5500	gacacatgcacagctggaaaanaaattgaanaccctaaagtaagtaaaccttaacattagca	5541
QY	4502	caattaaatagaataggtttctcttgattggaattcaatagctgtaatgctatgaag	4561
Dp	5540	caattaaatagaataggtttctcttgattggaattcaatagctgtaatgctatgaag	5581
QY	4562	acctatlaaaaaatctctcatagagccgtccctatccaaalgaatccctccttttg	4621
Dp	5780	acctatlaaaaaatctctcatagagccgtccctatccaaalgaatccctccttttg	5721
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Dp	5720	ctattcctctctttgtatagattgtaccagaataaataaagttgataatgctgcaatga	5661
QY	4682	gaagaataggaaatgctgtaaaacaatcaactctttaaaccctgttaagtcacaacatctg	4741
Dp	5660	gaagaataggaaatgctgtaaaacaatcaactctttaaaccctgttaagtcacaacatctg	5601
QY	4742	gclataatgtaactgagggaataalccaataagatatccacagactagaattaatatalt	4801
Dp	5600	gclataatgtaactgagggaataalccaataagatatccacagactagaattaatatalt	5541
QY	4802	tataagaagaagacccaanaactgtccagaatttgaagagtttaactatratatactaa	4861
Dp	5540	tataagaagaagacccaanaactgtccagaatttgaagagtttaactatratatactaa	5481
QY	4862	agcagtaactggaactggtgcatlttgacatcttgctccaaaccataatctgttcacaaat	4921
Dp	5480	agcagtaactggaactggtgcatlttgacatcttgctccaaaccataatctgttcacaaat	5421
QY	4922	ttataatgatacagaacccctaggcagagagaggaataatgaagtlccaaggaatgaaa	4981
Dp	5420	ttataatgatacagaacccctaggcagagagaggaataatgaagtlccaaggaatgaaa	5361
QY	4982	gaaaaatggggccctcctaattagctctctcctaattggcagtggttaagtttaact	5041
Dp	5360	gaaaaatggggccctcctaattagctctctcctaattggcagtggttaagtttaact	5301
QY	5042	agaaatgcagagcgtgtgttagcttggttagagtgagcagaagaacatgaaagatgtgtg	5101
Dp	5300	agaaatgcagagcgtgtgttagcttggttagagtgagcagaagaacatgaaagatgtgtg	5241
QY	5102	cagcgtcttlltaccacagccctgcctgcatatacaatgcaacccctcctctgatalttt	5161
Dp	5240	cagcgtcttlltaccacagccctgcctgcatatacaatgcaacccctcctctgatalttt	5181
QY	5162	gtcctcttagatgtctaaatactagatagcctttgtttgggttagattcaatttctc	5221
Dp	5180	gtcctcttagatgtctaaatactagatagcctttgtttgggttagattcaatttctc	5121
QY	5222	cacacatgatacccatltaaaaaaacaatgctcgtatgctgtctgtagatattcatatta	5281
Dp	5120	cacacatgatacccatltaaaaaaacaatgctcgtatgctgtctgtagatattcatatta	5061
QY	5282	gcccagatattctctctctgtgtgtatgacacagatagatcttgctcttctcgaagccctc	5341
Dp	5060	gcccagatattctctctctgtgtgtatgacacagatagatcttgctcttctcgaagccctc	5001
QY	5342	gttctgttaactaactcactctggacactataacaaaggaatccctcctaataaagca	5401
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QY	5402	tagaatgatacaaatgttcagaccgttgggttttaattctgtttagaacaatgtgcctcttc	5461
Dp	4940	tagaatgatacaaatgttcagaccgttgggttttaattctgtttagaacaatgtgcctcttc	4881
QY	5462	acaagtgtaacctgcctgataattatcttcttcttggttaataalaattccaaccttg	5521

D	4880	ACAAGTAACCGTCGTATTTATTTATTTCTTTTGGTAAATATTAATTTCCAAATTTTG	4821
Q	5532	tggtcagcagcgctcctaaggttacgtcacacagactgcaggttggatatagtcacgc	5583
D	4820	TGGTCAAGCAGCGGTAAAGGTTACGTACACACAGACTGCAGTTGGTATGTACAGCC	4761
Q	5582	aatcccttaataatgatacagatttgttaagacataataatggattcttagaag	5641
D	4760	AATCCCTCAATTAAATGATACAGATTTAATTAAGATATTAATTAAGATTTCTTGGAAG	4701
Q	5642	talpcccaatagaacttllataactaaagcgttggataaacatccatcagaaggaag	5701
D	4700	TATGCTCATAGAACTTTAATACTTTAAGCTTGTAAAAACATCCATGAAGGAAAG	4641
Q	5702	ctctcagcaatacgtcgtccaggyaataaggctaaataacatgaacataataatggtt	5761
D	4640	CTCTCAGCAATAACGCTCAGAGAAATAGGGCTAAATTAACGAACATTAATTAATGGTT	4581
Q	5762	aaagtgacgtttagtcgagcgctcaabgcttgcacaaagatgatatgtacaaggact	5821
D	4580	AAAGTGCTGCTTATAGTCGAGCCCTCAATCTTGTGCACAGAGATGTATGACAGACAGAT	4521
Q	5822	ttataalttgcatatalgtgccaaacagagttatlltttggcacagaaatgaa	5881
D	4520	TTATAATTTGCATTAATATGTGCCACACAGATTTATTTTGGCCAGAGATGTAGA	4461
Q	5882	agatattaacgctcctcgtgatgcacgtcgcagattaacttcatcctaagaagttgga	5941
D	4460	AGATATTACAGCTCTGGAAGCAGTCGATGATTAATTTATTTAATGAAGTTGGGA	4401
Q	5942	gaacaaataggaaaaaaaaacttalltctcagtaaatatlaatgattacttcaaa	6001
D	4400	GAACAAATAGGAAAAAAAACCTATTTTTCCTAGTAAATATTAATGATTTACATTTTCAAA	4341
Q	6002	taatggtgcctgaacatlttgataattatttctcaacgltgacatgacaaagaata	6061
D	4340	TAAATGGCTCAACTATTTGATTAATATTTATTTCTACAGTACGTAATGACAAATATAT	4281
Q	6062	lccatcatcatlaagtcagttctcgtctcgtcagcgtttacatttcagaaatgagc	6121
D	4280	TCCATATGCAATTAAAGTCATTTTGCGTCTGCTAGCTGTTTACATTTGCAAAATGTAGC	4221
Q	6122	aaacaagtaatgaagcaacatttctcatttgacatagatatacccttltgtgtgtgtg	6181
D	4220	AAACAAGTAATGAGCAACAATTTCTATTCAGATGACATTCCTTTGTGTGTGTGTG	4161
Q	6182	tgcattaagttgttaagcgaacatgaacaaagaacaaatgaaagtcttgcataatgataag	6241
D	4160	TGCATTAATAGCTTAAAGGTAACATGTAACAAATGAAGATTTCTGTATAATGTATGG	4101
Q	6242	aaacaagaagaagaatgaaatatttlltctgctacttagaanaaaaggtgtagacta	6301
D	4100	AAAAACAAGAAATGAAATATTTTATTTATGCTTACTTAGSAAAAAAGGATAGCATTA	4041
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D	4040	TTGATTTCCAAAGTAACTTTTATTTTAAATTTTAAAGCTTAACTGTAACATCATTTATGCTT	3981
Q	6362	aagatataaacaataataccctcttllatgtcttgcataagttatataatgaacatc	6421
D	3980	AAGATATTAATATATATCTCTTTTATTTATTTGCTTTGTATATGTTCAATGAACATTTCC	3921
Q	6422	agaataatttgataagtgltgctgtaaacctgcgaacgcgtatcttlltttgcattcgt	6481
D	3920	AGAAATTTATTTGATAAGTGTCTGTGAATGCAACGCTGATTTTATTTTGGCATTCGT	3861
Q	6482	agtcgaatttgacaccatttttaacttaattcgaagttgcttggatacatgttctgt	6541
D	3860	AGTCGATTTTGCATCCATTTTATTAATTAATTTTGCAGATGTGCTTTGATATATGTTTGTGTT	3801
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Qy 6902 gatgacatccaaatgtagtagcagactgagaggtgacaaatgaagatcctaagaag 6961
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Qy 6962 aggaagatcccccacaacaacatalttaatttcttagtaaaaaagaatacagaatgct 7021
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Qy 7022 cgtggcaatcccttaagcaacatatactatgtagctgttaaatcagcaaaaacacagaa 7081
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Db 3260 GTTGGTTAACTTGGGCAATATGCAAGTAACTTTTGGGCAAACTCTCATTAATAC 3201
Qy 7142 aattctcagtagtgcgacacaataagttccttatttcttgcacatgtagtgccttcta 7201
Db 3200 AATTCTCTAGTGTGTGCGACACAAATAGTCTTATTTTGGCAATGTATGCTTTTGA 3141
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US-10-092-400-6816/c
Sequence 6816, Application US/10092400
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC010C1
CURRENT APPLICATION NUMBER: US/10/092,400
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,874
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
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PRIOR APPLICATION NUMBER: 60/225,447
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PRIOR APPLICATION NUMBER: 60/216,647
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PRIOR APPLICATION NUMBER: 60/225,267
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PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065

Query Match Best Local Similarity 65.7%; Score 6774.6; DB 37; Length 10246;
Matches 6859; Conservative 0; Mismatches 26; Indels 40; Gaps 3;

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 ; FILE REFERENCE: PC010PCT
 ; CURRENT APPLICATION NUMBER: PCT/US01/01334
 ; CURRENT FILING DATE: 2001-01-17
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Qy 4502 caatlaaataagaataggcttcttgatgggaatccaatagctgtatgttcttataag 4561
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Db 5359 GCTAATATGTACTGGGAATATATCATTAAGATATCCAGACTAGAAATTAATAATAT 5300
Qy 4802 talaaagaagaagacaaactgtcagaattgaaaggttaacatattattataactaa 4861
Db 5299 TATAAAGAAAGACAAACCTCTAGCAATTTGAAAGGTTTACATATTTATTAATCA 5240
Qy 4862 aagcagctgactgacatgacatltgtlccaaacccataaattgttgcctaat 4921
Db 5239 ACGAGTACTGACCGGCATTTGACCATTTGTCCAAACCCATTAATTTGTGCTTAAT 5180
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Db 5179 TTAATATGATCAATAAACCTTAGCGAGAGAGAAATGAAGGTCCAGGCAATGAAA 5120
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Qy 5282 gcaaggtatttcttctgtgtgtgtagaaccagatgtagtcttcttcaagcctct 5341
Db 4819 GCGAGTATTTCTTTCTTGTGTGTATGACCAAGATGATGATTTGCTTAAGCTCCT 4760
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Db 4759 GTTGCTTACTAATCTACTTGGCACTTATTAATTAAGGAATCCCTCAATTCAAAAGCA 4700
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Db 4519 AATCCCTCAATTAATGTATACATTTAGTATGATGATTAATTAATGATTTGTAAG 4460
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Qy 8521 TTAAGT 8579
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Db 22 AGATGT 1

RESULT 11
US-09-764-874-6814/C
; Sequence 6814, Application US/09764874
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010
; CURRENT APPLICATION NUMBER: US/09/764,874
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11

1	PRIOR APPLICATION NUMBER: 60/225,447
2	PRIOR FILING DATE: 2000-08-14
3	PRIOR APPLICATION NUMBER: 60/218,290
4	PRIOR FILING DATE: 2000-07-14
5	PRIOR APPLICATION NUMBER: 60/225,757
6	PRIOR FILING DATE: 2000-08-14
7	PRIOR APPLICATION NUMBER: 60/226,868
8	PRIOR FILING DATE: 2000-08-22
9	PRIOR APPLICATION NUMBER: 60/216,647
10	PRIOR FILING DATE: 2000-07-07
11	PRIOR APPLICATION NUMBER: 60/225,267
12	PRIOR FILING DATE: 2000-08-14
13	PRIOR APPLICATION NUMBER: 60/216,880
14	PRIOR FILING DATE: 2000-07-07
15	PRIOR APPLICATION NUMBER: 60/225,270
16	PRIOR FILING DATE: 2000-08-14
17	PRIOR APPLICATION NUMBER: 60/251,869
18	PRIOR FILING DATE: 2000-12-08
19	PRIOR APPLICATION NUMBER: 60/235,834
20	PRIOR FILING DATE: 2000-09-27
21	PRIOR APPLICATION NUMBER: 60/234,274
22	PRIOR FILING DATE: 2000-09-21
23	PRIOR APPLICATION NUMBER: 60/234,223
24	PRIOR FILING DATE: 2000-09-21
25	PRIOR APPLICATION NUMBER: 60/228,924
26	PRIOR FILING DATE: 2000-08-30
27	PRIOR APPLICATION NUMBER: 60/224,518
28	PRIOR FILING DATE: 2000-08-14
29	PRIOR APPLICATION NUMBER: 60/236,369
30	PRIOR FILING DATE: 2000-09-29
31	PRIOR APPLICATION NUMBER: 60/224,519
32	PRIOR FILING DATE: 2000-08-14
33	PRIOR APPLICATION NUMBER: 60/220,964
34	PRIOR FILING DATE: 2000-07-26
35	PRIOR APPLICATION NUMBER: 60/241,809
36	PRIOR FILING DATE: 2000-10-20
37	PRIOR APPLICATION NUMBER: 60/249,299
38	PRIOR FILING DATE: 2000-11-17
39	PRIOR APPLICATION NUMBER: 60/236,327
40	PRIOR FILING DATE: 2000-09-29
41	PRIOR APPLICATION NUMBER: 60/241,785
42	PRIOR FILING DATE: 2000-10-20
43	PRIOR APPLICATION NUMBER: 60/244,617
44	PRIOR FILING DATE: 2000-11-01
45	PRIOR APPLICATION NUMBER: 60/225,268
46	PRIOR FILING DATE: 2000-08-14
47	PRIOR APPLICATION NUMBER: 60/236,368
48	PRIOR FILING DATE: 2000-09-29
49	PRIOR APPLICATION NUMBER: 60/225,856
50	PRIOR FILING DATE: 2000-12-08
51	PRIOR APPLICATION NUMBER: 60/225,868
52	PRIOR FILING DATE: 2000-12-08
53	PRIOR APPLICATION NUMBER: 60/229,344
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55	PRIOR APPLICATION NUMBER: 60/224,997
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57	PRIOR APPLICATION NUMBER: 60/229,343
58	PRIOR FILING DATE: 2000-09-01
59	PRIOR APPLICATION NUMBER: 60/229,345
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62	PRIOR FILING DATE: 2000-09-01
63	PRIOR APPLICATION NUMBER: 60/229,513
64	PRIOR FILING DATE: 2000-09-05
65	PRIOR APPLICATION NUMBER: 60/231,413
66	PRIOR FILING DATE: 2000-09-08
67	PRIOR APPLICATION NUMBER: 60/229,509
68	PRIOR FILING DATE: 2000-09-05
69	PRIOR APPLICATION NUMBER: 60/226,367
70	PRIOR FILING DATE: 2000-09-29
71	PRIOR APPLICATION NUMBER: 60/237,039
72	PRIOR FILING DATE: 2000-10-02
73	PRIOR APPLICATION NUMBER: 60/237,038
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PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,080
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,063
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,397
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,399
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,401
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/241,808
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,826
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,786
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,221
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/246,475
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: 60/231,243
PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,398

Query Match 63.9%; Score 6587.2; DB 30; Length 10004;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 6657; Conservative 0; Mismatches 13; Indels 12; Gaps 5;

Qy 3422 gactccagcgcttaacatcatatacaaaacggygagagattatagagag 3481
Db 6679 GATCCAGCCCTTTAAACATCAATAACAAACACGGTACAGATTATTAAGAGAG 6620

Qy 3482 aacaagaagcgcttaacccaagagcactcaagctgaagcactcaacaacagag 3541
Db 6619 AACAGAAAGCGCTTAACCCAAGGCACTTAGGCTAGAGCTCAACAAACAGCAG 6560

Qy 3542 gggcgcaatgagagcaagtcabggaagccgttagagagaggtcagagatcat 3601
Db 6559 GGGCAGCAATGAGAGCAAGTCAATGGAAGCCGTTAGAGAGAGGTCAAGAAATCATCT 6500

Qy 3602 aactgaagtcacagagagaattccactcccgagcctaagtaaatagagccaggg 3661
Db 6499 AACTGAAGTCAACAGAGAAATTCACCTCCCGCCTAAGTAATAGCAAGCCAGGG 6440

Qy 3662 ttaactgaactaaagcactctgctcaagcagctcctggtcagccaactctgatat 3721
Db 6439 TTTCATTGACTAAAGCCATTCTGCTCAGCAGCAATCCTGTCACGCAAACTCTGATAT 6380

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Qy 3782 tccaggaatagttcatcgatctgaaaggaagaagttctggaagagagagccctat 3841
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Db 6199 AAAGTACCAATGACCACTTTTGGACTTCCTCTTGATACATTAATGACTTCCAGAGTGAAGC 6140

Qy 3962 tgaatgctggcggttcctgagtaataatgaactccctgcttcttgggaatccgaactact 4021
Db 6139 TGATTTGGCTGGCGTTCTGTGAGTAATTAAGCTCTCCGTTCCGTGGAACTCCGACTACTT 6080

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Qy 4082 tctgctccctcatlttcaagctgttgatcagacaatgcaatccctctcctatgttggcat 4141
Db 6019 TCTGCTCCCTCATTTTTCAGCTGTGATGATGACATGACATTCCTCTAGATTITGGCGAT 5960

Qy 4142 caagcattccagactgggccaactgcaaaaggttgcctcccaagagaaaacgaagagacc 4201
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Db 5899 ACCCAATGTAAAAATGAAAGTCCCTTGAATGTATTAATAACAGAAAGTTGATGAAAG 5840

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Db 5599 CAATTAATAATAGAAATAGTCTTTCTTGATGGAAATCAATAGCTGTATGCTTAAGAG 5540

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DB 22 AGATCATTTGTAATATATATA 1

RESULT 12
US-10-092-400-6814/c
Sequence 6814, Application US/10092400
GENERAL INFORMATION:
APPLICANT: rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC010CI
CURRENT APPLICATION NUMBER: US/10/092,400
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 09/764,874
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496

PRIOR FILING DATE: 2000-07-11
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 PRIOR APPLICATION NUMBER: 60/246,475
 PRIOR FILING DATE: 2000-11-08
 PRIOR APPLICATION NUMBER: 60/231,243
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/233,065

Query Match 63.9%; Score 6587.2; DB 37; Length 10004;
 Best Local Similarity 99.6%; Pred. No. 0;
 Matches 6657; Conservative 0; Mismatches 13; Indels 12; Gaps 5;

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 QY 3482 aacagaagaagcgcttaaccagagcgacttagctgagcagtaacaacagcagag 3541
 Db 6619 AACAGAAGAAGCGCTTAACCAAGGACTTGAAGGAGGAGGAGGAGGAG 6560
 QY 3542 gggcagcaatgagagcaagtcacatgaaagccgttagagagagggtcagaagatcatct 3601
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GENERAL INFORMATION:			
APPLICANT: Human Genome Sciences, Inc., et al.			
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies			
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2	PRIOR FILING DATE: 2000-07-14
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5	PRIOR APPLICATION NUMBER: 60/226,868
6	PRIOR FILING DATE: 2000-08-22
7	PRIOR APPLICATION NUMBER: 60/216,647
8	PRIOR FILING DATE: 2000-07-07
9	PRIOR APPLICATION NUMBER: 60/225,267
10	PRIOR FILING DATE: 2000-08-14
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13	PRIOR APPLICATION NUMBER: 60/225,270
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34	PRIOR APPLICATION NUMBER: 60/215, 135	
35	PRIOR FILING DATE: 2000-06-30	
36	PRIOR APPLICATION NUMBER: 60/225, 266	
37	PRIOR FILING DATE: 2000-08-14	
38	PRIOR APPLICATION NUMBER: 60/249, 218	
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56	PRIOR APPLICATION NUMBER: 60/249, 215	
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68	PRIOR APPLICATION NUMBER: 60/233, 081	
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PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/233,065
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,398

Query Match 56.2%; Score 5793; DB 1; Length 5825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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3482 aacaaagaagcgcttaaccagagagcactcaggtcgagcaactaaacaacagcagag 3541
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3542 gggcagcaatgagagcaagctcaatggaagccgcttagagagaggtcagaagatcatc 3601
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DB 5 TTTT 1

RESUME 14
US-09-764-874-6815/c
; Sequence 6815, Application US/09764874
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010
; CURRENT APPLICATION NUMBER: US/09/764,874
; CURRENT FILING DATE: 2001-01-17

PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR FILING DATE: 2000-07-11
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PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,398

Query Match 56.2%; Score 5793; DB 30; Length 5825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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3482 aacaagaagcgtcttaaccagagcacttcagctgagcagctcaacaacagcagag 3541
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5765 AACAGAAACCGCTTTAACCCAGAGGCACTTCACTGAGCAGCTCAACAAACAGAGAG 5706
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3542 ggagcagaatgagagcaagcaatgagagcccgtaagagagaggtgcagaagatcat 3601
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5705 GGGAGCAGATGAGAGAGCAAGTCAATGAGAACCCGTTAGAGAGAGGTCAGAAATCATCT 5646
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3602 aactgaagaatcaccaagagaaatlcacatcccaagccctaaagtaataagaacccaag 3661
|||||
5645 AACGAAAGTCACAGAGAGAAATTCACATCCCAACCTTAAGTAAATPCCAGAGCCAGAG 5586
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3662 ttattgactaaagcactctgctcagcagcagctccgtggtgcagccaactgtgatal 3721
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5585 TTCAATGACTAAAGCCATTTCTGCTCAGCAGCAGCTGCTGATCAGCAAACTGTGATAT 5526
|||||
3722 tcacaaagaatgacaccttgacacatcagtaataaagttcctcagaagaagtactgaga 3781
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5525 TCACAAAAGATGCAACCTTTGCACTTCAGATTAAGAAAAATCTCTCAGAAAGTACTGAGA 5466
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3782 tccaggaataagttatcctcgtatctgaaggaaagaatctcagaagagcgtccat 3841
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5465 TCCAGGAATTAAGTTATCCGATATCTGAAGGAGAAAGAGTTCTGAGAGAGCAGTCTAT 5406
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3842 agaaagatcatgagacctgcgaacacccaattatcacacccaagagccacttga 3901
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5405 AGAAAGTACATGAGAGACTGCGAAACACCAAAATTAATACACAGAGCCCTTTGA 5346
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3902 aaagtccagatccactcttttggactcccttgactacataaagactccagaagtga 3961
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5345 AAAGTACCAATGACCACTTTTGGACTCCCTTTGATTAATGACTTCCAGAGTGAAC 5286
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3962 tgattgcgcggttctgagtaataataagctcccgctccgtggagatccgactact 4021
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5285 TGATTTGGCTGGCTTCTGGAGTAAATATTAAGCTTCCTGGGATCCGACACTT 5226
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5225 GAGTCAGTGCTGGCTTACCAAAATCCTTGCCAAATATGTGCTTATCCACTTCA 5166
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4082 tctgctcctcctatttttcaagctgttgatcagacaagatccctctagattgagat 4141
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5165 TCTGCTCCTCATTTTTCACCTGTTGATTCAGACATGACATTCCTTATGATTTGGCAT 5106
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4142 caagcatlccagacctgagccaactgcaaggtgcctccagaagaaacgaagcacc 4201
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5105 CAAGCATTCAGACCTGGCCCACTCCAAACGGTCCCTCCAGAGAGAAACGAGGACAC 5046
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4202 accaaatgtaaaaaatgaagctccctgaatgtagtaaaaaagagagaaagttagaag 4261
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5045 ACCAAATGTAAAAATGAAGTCCCTTGAATGATTAAGAAAGAGAAATGATAGAG 4966
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4262 tactcaagataaacttcaacaaatggtgactcgtggaactgtcttcgtgtaga 4321
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4985 TACTCAATTAACCTTCAACAAATGTTGACGTGCGATGCTCTTCTGATGAGAGT 4926
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4322 gatgtagcttgatagtagtgcagagtgacagtgagaccccttcagtgagatg 4381
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4925 GATGATGCTTGGATATAGAGTTGCCATGCGACAGTGGACCTTCCAGTGGAGATAG 4866
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4382 ccagatcttgcagagcaaatatgactcaacaacatatccagaagggtccgtag 4441
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4865 CCAGATCTTTGACAGGACAAATATGACTTCACAAACATATCCAGAGGCGCTGACAT 4806
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4442 gaacaaagcaagtgaaaaaaatgaaacccaagagtaaaccttagcacttagca 4501
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4562 accatataaaaaataactcatagagcctgactatccaacatgaatctccctcttg 4621
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4685 ACCTATTAAAAAATCTTCATAGAGCTGCTTATCAAAATGAATTCCTCTTTTG 4626
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4682 gaaagaaatgaaatgtaaaacaatctttaaaccgttgaagtaaaacatcttg 4741
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4565 GAAAGAAATGGAAGATGTAACAAATCACTTTTAAACCTGTTAAGTCAAAACCATTTG 4506
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4742 gctatatgactcggggaataatcacaagagataccagactagataatataat 4801
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4802 tataaagaagaacccaactgctagatlttgaagggtttaaataataataata 4861
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Db 4445 TATAAGAAAGAGCAAAACCTGTAGATTGAAAGGTTTCATATTATTATACCTAA 4386
Qy 4862 agcagtaactgagctggccatctggacattgttccaaaaccataaattgttcctaact 4921
Db 4385 AGCAGTACTGGACGGCCACTTGCACCATTTGTTCCAAAACCATTAATTTGTCCTAAAT 4326
Qy 4422 ttataatgataaaccctgagcagagagagaaattgaaagtcagggaalgaaa 4981
Db 4325 TTATATATCATGATAAACCTAGCAGAGAGAGAAATGTAAGTCCAGGCAATGAAA 4266
Qy 4982 gaaaatggcgccctcccaattagctctctctatctgagcattgttcgaatttgcact 5041
Db 4265 GAAAAATGGCCGCTCTCAATTTAGTCTCTCTCATTTGCGCATGTTTCAGATTTTGACT 4206
Qy 5042 agaatggcagctgtgtttagcttgtagagtgacgaagaacaatgacagatgagtg 5101
Db 4205 AGAAATGGACCTGTGTAGCTGTGTAGAGTGCACCAAGCAACATGACAGATGTGCG 4146
Qy 5102 cagcgtgtttttacccagcccgccgtgatacaatgacatgcaacctctctgatalttt 5161
Db 4145 CAGCGTGTGTTTACCCAGCCCTGCCGTACATGACATGCAACCCCTCCTCATATTTT 4086
Qy 5162 gtcccttagatgttcaaatctcagtagtcccttggtttgggttttagatttatttgc 5221
Db 4085 GTTCCTTTAGATGTTCAAAATCTAGTAGTCTTTGTTGGGTTTATGATATTTTGTG 4026
Qy 5222 caacatgtaaccaatttaaaaaaacaatgtccagatgtctctgtatgatttcaattt 5281
Db 4025 CACACATGTACCCATTTTAAAAAACAATGCTCGATGCTTGTGATGATTTTCAATTTT 3966
Qy 5282 gccagatattcttctgtgtgtgtatgacagatagattgttcttcttaagctct 5341
Db 3965 GCGAGGTATTTCTTTCTTTGTTGTGTGATGAAACCATGATGATGATTTGCTTTCTAAGCCCT 3906
Qy 5342 gtgtgttaactatctcaactgtggcaattaaactaaagaaatcccttaactaaaca 5401
Db 3905 GTTGGTTACTATCTCACTTGGACATTTTAACTTAAAGAAATCCCTCATTTCAAAACA 3846
Qy 5402 tagatgatacaaatgtcagaccgtgtgttaattgttttagaacaatgagattcttc 5461
Db 3845 TAGATGATATCAAAATGTCAAGCGTGGTTTAAATGTTTAAAGAACATGGCATTTCTTC 3786
Qy 5462 acaagtaactgtgtatatttatttatttcttctgttataataatttccaacttg 5521
Db 3785 ACAGAGTACCTGCTGATTTATTTATTTTCTTTGGTTAAATTAATTTCCAAACTTGG 3726
Qy 5522 tggtaagcagcgttctaagttacgttaccacagacgtgagattgttatatccacc 5581
Db 3725 TGGTACGAGCAGCGTCTAAGGTTACGTTACACAGACTGACAGTTGATATATACCAACC 3666
Qy 5582 aatcccttcaataatgtatacaagattagtaagtaacataatagattcttagaag 5641
Db 3665 AATCCCTTCATTAATGTATACAGATTAGTTAAGTTCATTAATAGATTTCTTAAAG 3606
Qy 5642 tatgtccatagaactttaacttaagctttagtaaaactatccatgaaggaag 5701
Db 3605 TATGTCCCATAGACTTTTAAATACTTAAGCTTTGTAATAACTATCCATGTAAGGGAAG 3546
Qy 5702 ctccctcagcaatactgtcaggaataagggctaataaactgtgaacttaataatggt 5761
Db 3545 CTCCCTCAGCAATACTGCTCAGGAAATAGGGCTAAATACATGACATTTAATTTGTT 3486
Qy 5762 aaagtgtcgtatgtcagcactcaatgtctgtcacaagaatgtatgtatcaagaactgact 5821
Db 3485 AAAAGTGCTGTAGTGCAGCCCTCAATGCTGTCTACAGATGTATGTACAGAGACTGACT 3426
Qy 5822 ttaataattggcatatattgtcccaaccagtagttatttcttgcacagagatgtaga 5881
Db 3425 TTAAATATTTGCAATTAATTTATTTGCCAACCACTAGTTATTTTGTGCGAGAGATGTAGA 3366
Qy 5882 agatataaagtaactgactgtcagatgtcaatgaactatttcatcttaaaagattgga 5941
Db 3365 AGAATATACAAAGTACTGATGCTGACACTGTGACATTAACCTATTTCATTAAAGAAAGTGGGA 3306

Qy 5942 gaacaaataggaaaaaaaaaaactatttcttctagtaaatatgattacatttcaaa 6001
Db 3305 GAACAAATAGGAAAAAATATTTTCTAGTAAATATTAATGATTAATTCATTTCAAA 3246
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Db 3245 TAATGTGCTCCTACATATTGATTAATTAATTTCTTACAGTACGATGACAAATATAT 3186
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Db 3185 TCCATCATCATTTAGACATGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3126
Qy 6122 aaaaaggtgaatgaagcagcaacttctcatgtcagatagatacccttgtgtgtgtgt 6181
Db 3125 AAAACAAGTAATGAAGCAACATTTTATTTGCAATGATGATGATGATGATGATGATG 3066
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Db 2885 AAGATGATTAACATTAATCCCTTTTATTTATTTGCTTGTATGTTTCAATGAATCTTC 2826
Qy 6422 agaaattacttgaatgagttgtcgtgaatctgcagacgtat-cttttttgcattcg 6480
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Db 2705 TTGGGTTTGTGTTCTTTTCTTCTACAGTGGCGGCTTCGTTCTTAAATTTGATGGAGGT 2646
Qy 6601 agagtcaaacagttcgtcgtcgtgtgttagcgaatgaatgaatgaatgaatgaatga 6660
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Db 2465 TATTTGTATCTACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2406
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Db 2285 GAGGAGATTCCTCCCAACAAATATTTAATTTCTTATGTAATTAATTAATTAATTAATTA 2226

QY 7021 tcgtggaatccttaagcaaatatctatgtagctgtttaaactcagcaaaacaccaga 7080
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QY 7621 catgagatttgaagatttctctcttggaaagagctcccttgtagaagaattgtag 7680
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QY 7801 ttcttcaacttctctcactcaactcactctgattcattctgtgttggtagaaga 7860
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Db 1325 caagtataagaagaagaagagagagcttaattatgaactctgtagtcaagaagaaga 1266
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QY 9120 agaaagaagaagaatcaacttgaactgaagaatgttgaacttataagaagaatgtg 9179
Db 125 agaaagaagaagaatcaacttgaactgaagaatgttgaacttataagaagaatgtg 66
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Db 5 ttttt 1

RESULT 15
US-10-092-400-6815/c
; Sequence 6815, Application US/10092400
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC010CI
; CURRENT APPLICATION NUMBER: US/0/092,400
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,874
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/224,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
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; PRIOR APPLICATION NUMBER: 60/229,344
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; PRIOR APPLICATION NUMBER: 60/234,997
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; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
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; PRIOR APPLICATION NUMBER: 60/229,509
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Query Match 56.2%; Score 5793; DB 37; Length 5825;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5818; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

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QY 3662 ttattgactaaagcaattctgctcagcagccagtcctgagcagcaacttgatat 3721
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D 2765 TATGTCATTTGCACTCCATTTTATTAATTTTGAATTTGCAAGTCTTTGATATGTTTGT 2706
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RESULT 2
PCT-US02-19669-471

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; Sequence 471, Application PC/TUS0219669
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038PC
; CURRENT APPLICATION NUMBER: PCT/US02/19669
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887

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; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 471
; LENGTH: 10011
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US02-19669-471

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Query Match 97.1%; Score 10011; DB 1; Length 10011;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10011; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dh	2821	agggacggttcaatgcatatccacatccaaagaagagcccaaaaattgacttcaaggtctaca	2880
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[illegible]

Query Match	9.1%;	Score 943.4;	DB 5;	Length 966;
Best local Similarity	99.7%;	Pred. No. 2.4e-159;		
Matches 966;	Conservative 0;	Mismatches 1;	Indels 2;	Gaps 2

	Coordinates	Conserved	Mismatches	Indels	Gaps
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Db	29	gctactgagtcagcctgcagta	taactatttcaataagaagcttgggaacaataag	88	
QY	5953	aaaaaaaaaactattttctcag	aaataataatgatatacatcattccaataaaytgcct	6012	
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QY	6013	gacatattgaataatattttct	cagtgacgtatgcaaaagaatattccatgcga	6072	
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QY	6073	ttgaatcagcttcggccttcgc	ctcagctgttcaactttgcaaatgtagcaacaaggtaa	6132	
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QY	6133	tgaagcaactatttctatgag	agataacctttgtgtgtgtgtgtgtgcattaagt	6192	
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RESULT      6
US-09-602-148A-31
: Sequence 31, Application US/09602148A
: GENERAL INFORMATION:
: APPLICANT: Mitcham, Jennifer L.
: APPLICANT: Jiang, Yugu
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
: FILE REFERENCE: 210121.482
: CURRENT APPLICATION NUMBER: US/09/602,148A
: CURRENT FILING DATE: 2002-04-09
: NUMBER OF SEQ ID NOS: 126
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 31
: LENGTH: 674
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-602-148A-31

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	Query Match	6-5%	Score 668.8	DB 5	Length 674
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Db 342 aaacccagaggttggtaacttgggaatatagcaagatattcttctgggcaaac 401
Qy 7131 actcattaagcaatctctcgaatgctgcgacacaaatagttcttattttggcagt 7190
Db 402 actcattaagcaatctctcgaatgctgcgacacaaatagttcttattttggcagt 461
Qy 7191 atgcctttatttccatcaatt 7215
Db 462 atgcctttatttccatcaatt 486

RESULT 9
US-09-918-995-10414
Sequence 10414, Application US/09918995
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10414
LENGTH: 476
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(476)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-10414

Query Match 4.2%; Score 435.8; DB 5; Length 476;
Best Local Similarity 97.1%; Pred. No. 1.2e-68;
Matches 440; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 4661 agcgagataatgctcaatgagaagatggaagatggttaaacatcaacttttaaac 4720
Db 24 agcgancctcncagncmcngagaagaatggaagatggttaaacatcaacttttaaac 83
Qy 4721 tcttaagtcataaacatcttgctaatactgactggggaataatccataagatata 4780
Db 84 tcttaagtcataaacatcttgctaatactgactggggaataatccataagatata 143
Qy 4781 ccagactgaatataatattataaagaagaagacccaacatgctlagaatttgaag 4840
Db 144 ccagactgaatataatattataaagaagaagacccaacatgctlagaatttgaag 203
Qy 4841 gttacataatataatataaagaagatgactggccatggaacattgttccaana 4900
Db 204 gttacataatataatataaagaagatgactggccatggaacattgttccaana 263
Qy 4901 cccataaattgttgcctaattataaalgatcatgaaacctagcgagagagagaat 4960
Db 264 cccataaattgttgcctaattataaalgatcatgaaacctagcgagagagagaat 323

Qy 4961 tgaagtcagggacatgaagaaaaatggcgccctccatattagcttctcattgg 5020
Db 324 tgaagtcagggacatgaagaaaaatggcgccctccatattagcttctcattgg 383
Qy 5021 ccatgttccaatgttgaactagaatgcagctgtggttaggtgttgaagtgagc 5080
Db 384 ccatgttccaatgttgaactagaatgcagctgtggttaggtgttgaagtgagc 443
Qy 5081 aagcaatgcagatggttggcagcgtgttt 5113
Db 444 aagcaatgcagatggttggcagcgtgttt 476

RESULT 10
US-09-918-995-19024/c
Sequence 19024, Application US/09918995
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19024
LENGTH: 379
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-19024

Query Match 3.6%; Score 374.8; DB 5; Length 379;
Best Local Similarity 99.5%; Pred. No. 9.2e-58;
Matches 376; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8751 gcaaatgagaagaatagaaagacgcccgcggaacttggagggcatgttattcc 8810
Db 378 gcaaatgagaagaatagaaagacgcccgcggaacttggagggcatgttattcc 319
Qy 8811 caaagaagaagcggcgaagcagagcatggaattcttgcagacacttcotttggtt 8870
Db 318 caaagaagaagcggcgaagcagagcatggaattcttgcagacacttcotttggtt 259
Qy 8871 ttcagtaacttccatagacagtggtgcacatgttccatagatgctgcaggttgc 8930
Db 258 ttcagtaacttccatagacagtggtgcacatgttccatagatgctgcaggttgc 199
Qy 8931 aaagcatcccaatgaatgcaatgaatgaatgaatgaatgaatgaatgaatga 8990
Db 198 aaagcatcccaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 139
Qy 8991 tcaagtatgcacatgaagaatgtaaatgaatgaatgaatgaatgaatgaatga 9050
Db 138 tcaagtatgcacatgaagaatgtaaatgaatgaatgaatgaatgaatgaatga 79
Qy 9051 acaatgtacatcatgtgtctcttgaagaagaagagagctgttaacttcaactgtc 9110
Db 78 acaatgtacatcatgtgtctcttgaagaagaagagagctgttaacttcaactgtc 19
Qy 9111 ctacacggagaaaagca 9128
Db 18 ctacacggagaaaagca 1

RESULT 11
US-09-539-800C-18053
Sequence 18053, Application US/09539800C
GENERAL INFORMATION:
APPLICANT: Seligman, Jeffrey J.
APPLICANT: Deleane, Angelo M.

```
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullaly, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
PRIORITY FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/943,979
PRIOR FILING DATE: October 4, 1997
PRIOR APPLICATION NUMBER: 60/027,782
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 18053
LENGTH: 314
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incycle ID No: hu01112257
US-09-539-800C-18053
```

```
Query Match 2.9%; Score 296.4; DB 5; Length 314;
Best Local Similarity 98.0%; Pred. No. 9.2e-44;
Matches 300; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6465 ttttttgcattcgtgtagtcgacattgcacatcatttaataatcgcagttgctt 6524
DB 9 ttttttgcattcgtgtagtcgacattgcacatcatttaataatcgcagttgctt 68
QY 6525 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttt 6584
DB 69 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttt 128
QY 6585 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgttgagcgaatgaatgaataa 6644
DB 129 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgttgagcgaatgaatgaataa 188
QY 6645 aatgtcttcctgagtcgtgtgtgttcatttcatttttgcatttttttttttttttttttt 6704
DB 189 aatgtcttcctgagtcgtgtgtgttcatttcatttttgcatttttttttttttttttttt 248
QY 6705 aaaaaagagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaa 6764
DB 249 aaaaaagagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 6764
QY 6765 catgtc 6770
DB 309 catgtc 314
```

```
RESULT 12
US-09-539-800C-17062
Sequence 17062, Application US/09539800C
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Deleage, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CONNECTIVE TISSUE
FILE REFERENCE: PD-1023 CIP
CURRENT APPLICATION NUMBER: US/09/539,800C
PRIORITY FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/521,383
PRIOR FILING DATE: August 16, 1995
PRIOR APPLICATION NUMBER: 08/271,217
PRIOR FILING DATE: June 27, 1994
PRIOR APPLICATION NUMBER: 08/334,881
PRIOR FILING DATE: November 4, 1994
PRIOR APPLICATION NUMBER: 08/943,978
PRIOR FILING DATE: October 3, 1997
PRIOR APPLICATION NUMBER: 60/028,732
PRIOR FILING DATE: October 4, 1996
PRIOR APPLICATION NUMBER: 08/993,774
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/034,975
PRIOR FILING DATE: December 20, 1996
PRIOR APPLICATION NUMBER: 09/250,003
PRIOR FILING DATE: February 10, 1999
PRIOR APPLICATION NUMBER: 60/074,364
PRIOR FILING DATE: February 12, 1998
PRIOR APPLICATION NUMBER: 09/452,747
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: 60/111,910
PRIOR FILING DATE: December 10, 1998
NUMBER OF SEQ ID NOS: 19698
SOFTWARE: PERL Program
SEQ ID NO 17062
LENGTH: 302
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incycle ID No: hu01255098
US-09-539-800C-17062
```

```
Query Match 2.9%; Score 294; DB 5; Length 302;
Best Local Similarity 100.0%; Pred. No. 2.5e-43;
Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6465 ttttttgcattcgtgtagtcgacattgcacatcatttttaataatcgcagttgctt 6524
DB 9 ttttttgcattcgtgtagtcgacattgcacatcatttttaataatcgcagttgctt 68
QY 6525 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttt 6584
DB 69 tgcataattgtttgttggttttttttttttttttttttttttttttttttttttttt 128
QY 6585 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgttgagcgaatgaatgaataa 6644
DB 129 aagttgagtcgagtcgagtcgacacacagtcgtagcgtgttgagcgaatgaatgaataa 188
QY 6645 aatgtcttcctgagtcgtgtgtgttcatttcatttttgcatttttttttttttttttttt 6704
DB 189 aatgtcttcctgagtcgtgtgtgttcatttcatttttgcatttttttttttttttttttt 248
```

QY 6403 ttttttttgatctctgtaagtcgaatttgacatccattttaacttaatttcgaattgctt 6524

Db 9 ttttttttgatctctgtaagtcgaatttgacatccattttaacttaatttcgaattgctt 68

QY 6525 ttttttttgatctctgtaagtcgaatttgacatccattttaacttaatttcgaattgctt 6584

Db 69 ttttttttgatctctgtaagtcgaatttgacatccattttaacttaatttcgaattgctt 128

QY 6585 aagtttgatagcgagtgagtttcaacaacgcttctgacactgtgtaagcagaatgaattaa 6644

Db 129 aagtttgatagcgagtgagtttcaacaacgcttctgacactgtgtaagcagaatgaattaa 188

[illegible]

	Query Match	2.48;	Score 251;	DB 5;	Length 253;
	Best Local Similarity	99.2%;	Ped. No. 1.2e-35;		
	Matches 251;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY	9758	ggaagatcttcattcgttgcctaagaanaagatccaatttgtagtgcctcgatttgaatactagg	9817		
Db	1	ggatgatcttcattcatgttcctaagaanaagattccaatcttgagtcgcgatcttgaatactagg	60		
QY	9818	aagtttggtcataataagtcttgtctcttcaacaacacatgaaaactlltttcgtttattcllantt	9877		
Db	61	aagtttggtcataataagttctgtgtncttcaacaacacatgaatrrtttttcgtttattcllantt	120		
QY	9878	tgtgtttcataagtcgaatgtctcaattctctaccacaacatgcttctgtgtatllctcltaag	9937		

Db 121 ttgtttctagtcgcatgltcaatttctaactcaacaacatgltcttggtgatttctatg 180
 Oy 9938 caaacatcttcaagcgaagaagtgtcgttacaatcctaaacttgaaataaagttta 9997
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 caaacatcttcaagcgaagaagtgtcgttacaatcctaaacttgaaataaagttta 240
 Oy 9998 ccaccagttacac 10010
 ||||||||||||||
 Db 241 ccaccagttacac 253

Search completed: July 22, 2002, 01:15:30
 Job time: 25977 sec

GenCore version 4.5
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OM nucleic - nucleic search, using SW model

Run on: July 21, 2002, 14:58:48 ; Search time 12014.9 Seconds
(without alignments)
17965.795 Million cell updates/sec

Title: US-09-702-216-1
Perfect score: 10315
Sequence: 1 ttctccgcgcgaaggtctcctt.....gtttatttcaaaaaaaaaa 10315

Scoring table:

IDENTITY-NWC
Gapop 10.0, Gapept 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Genbank1:
1: gb_da:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pal:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
------------	-------	-------	--------------	-------	-------------

1	10011	97.1	10011	9	AF183810	AF183810 Homo sapi
2	6756.2	65.5	16813	2	AC013815	AC013815 Homo sapi
3	6595.6	63.9	15905	2	AC023142	AC023142 Homo sapi
4	5295	51.3	5507	9	AF264784	AF264784 Homo sapi
5	3491.2	33.8	4452	10	AF346836	AF346836 Homo sapi
6	2486.4	24.1	2596	5	AK009948	AK009948 Mus muscu
7	2295	22.2	4625	5	AF346838	AF346838 Homo sapi
8	1580.6	15.3	1587	9	AK021511	AK021511 Homo sapi
9	1537	14.9	1551	9	AK021470	AK021470 Homo sapi
10	1423	13.8	165191	2	AC103571	AC103571 Rattus no
11	1306	12.7	3767	5	AF346837	AF346837 Xenopus 1
12	1139.4	11.0	82724	2	AC084171	AC084171 Homo sapi
13	1139.4	11.0	310002	9	AF178030	AF178030 Homo sapi
14	1116	10.8	165191	2	AC103571	AC103571 Rattus no
15	943.4	9.1	996	6	AK067304	AK067304 Sequence
16	771.2	7.5	113725	2	AC108615	AC108615 Rattus no
17	761.4	7.4	766	6	AX113088	AX113088 Sequence
18	668.8	6.5	674	6	AX067327	AX067327 Sequence
19	460.8	4.5	350000	9	AF130342	AF130342 Homo sapi
20	457.6	4.4	113725	2	AC108615	AC108615 Rattus no
21	275.4	2.7	305	6	AX156253	AX156253 Sequence
22	258.4	2.5	67407	2	AC013789	AC013789 Homo sapi
23	94	0.9	82724	2	AC084171	AC084171 Homo sapi
24	93.4	0.9	67407	2	AC013789	AC013789 Homo sapi
25	89.4	0.9	22448	2	PFMALP4	PFMALP4 Sequence
26	81.8	0.8	53932	2	AC023371	AC023371 Homo sapi
27	79.4	0.8	7355	6	AX344889	AX344889 Sequence
28	79.4	0.8	130540	6	AX079417	AX079417 Mus muscu
29	79.2	0.8	349980	6	AX344563	AX344563 Sequence
30	78.8	0.8	321003	2	PFMALP3	PFMALP3 Sequence
31	78.4	0.8	8079	6	AX356488	AX356488 Sequence
32	77.8	0.8	4865	3	AF364131	AF364131 Anopheles
33	77.8	0.8	12405	6	AX251840	AX251840 Sequence
34	77.8	0.8	12405	6	AX227872	AX227872 Sequence
35	77.8	0.8	12405	6	AX323555	AX323555 Sequence
36	77.8	0.8	22243	3	PFVAR21A	PFVAR21A Sequence
37	77.4	0.8	5126	6	AX348926	AX348926 Sequence
38	77.4	0.8	83440	2	AC024285	AC024285 Homo sapi
39	77	0.7	192929	2	AC005505	AC005505 Plasmodi
40	77	0.7	256172	2	AC005139	AC005139 Plasmodi
41	77	0.7	310779	2	AC005140	AC005140 Plasmodi
42	76.8	0.7	349980	6	AX344566	AX344566 Sequence
43	76.6	0.7	1141	6	AX083744	AX083744 Sequence
44	76.4	0.7	184535	2	CNS057CJ	AL355100 Homo sapi
45	76.2	0.7	99003	2	AL390756	AL390756 Homo sapi

ALIGNMENTS

RESULT	1	10011 bp	mRNA	PR1 10-JAN-2000
AF183810				
LOCUS				
DEFINITION				
ACCESSION	AF183810			
VERSION	AF183810.1	GI:5684533		
KEYWORDS				
SOURCE				
ORGANISM				
	human.			
	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
	1 (bases 1 to 10011)			
REFERENCE				
AUTHORS				
	Momeni, P., Glockner, G., Schmidt, O., von Holtum, D., Albrecht, B.,			
	Gillesen-Kaesbach, G., Hennekam, R., Meinecke, P., Zabel, B.,			
	Rosenthal, A., Horsthemke, B. and Ludecke, H. J.			
	Mutations in a new gene, encoding a zinc-finger protein, cause			
	tricho-rhino-phalangal syndrome type I			
TITLE				
JOURNAL	Nat. Genet. 24 (1), 71-74 (2000)			
MEDLINE	20082812			
REFERENCE				
AUTHORS				
	Momeni, P., Glockner, G., Schmidt, O., von Holtum, D., Albrecht, B.,			
	Gillesen-Kaesbach, G., Hennekam, R., Meinecke, P., Zabel, B.,			

QY 1501 ctggctgctgcagagacatcaatctctcaaggccctgttttactaaatgaggactatgatg 1560
DB 1501 ctggctgctgcagagacatcaatctctcaaggccctgttttactaaatgaggactatgatg 1560
QY 1561 tgcaggctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgcag 1620
DB 1561 tgcaggctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgcagctgcag 1620
QY 1621 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1680
DB 1621 ggaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1680
QY 1681 cagaaatagaaacacatctctcagacccacacacacacacacacacacacacacacacac 1740
DB 1681 cagaaatagaaacacatctctcagacccacacacacacacacacacacacacacacacac 1740
QY 1741 cctcctgagcttgcagaaac 1800
DB 1741 cctcctgagcttgcagaaac 1800
QY 1801 ccagctgctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1860
DB 1801 ccagctgctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1860
QY 1861 acactcctgctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1920
DB 1861 acactcctgctgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1920
QY 1921 cagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1980
DB 1921 cagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1980
QY 1981 caactaaactgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
DB 1981 caactaaactgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2040
QY 2041 atccagagctaaatgaaagcttcccaaggcctctgcacatgaaatgaaatgaaatgaaatg 2100
DB 2041 atccagagctaaatgaaagcttcccaaggcctctgcacatgaaatgaaatgaaatgaaatg 2100
QY 2101 aaagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2160
DB 2101 aaagctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2160
QY 2161 agagctcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2220
DB 2161 agagctcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2220
QY 2221 gtagcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2280
DB 2221 gtagcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2280
QY 2281 gtagcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2340
DB 2281 gtagcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2340
QY 2341 ccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2400
DB 2341 ccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2400
QY 2401 gaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2460
DB 2401 gaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2460
QY 2461 gaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2520
DB 2461 gaaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 2520
QY 2521 taactcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2580
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QY	5941	agacaaataggaagaaaaaaactattttctcagtaaatatataatgtatthacatllcaa	60000
Db	5941	AGAACAAATAGGAAAAAAACCTATTTTCTTAGTAATATTAATTAATGATTAATTCATTC	60000
QY	6001	ataatggtgctgcacathtgataataattattctcagatgtacagtaatgtgaagaaagata	60600
Db	6001	ATPAAGTGGCTGCATATTTGAAATATATTTCCTACACTGACGCTATGCACAAAGATA	60600
QY	6061	tlccatcatgcatatagagtcagatctctggctctgcctaagctgttllacatctgcacatgta	61200
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QY	6121	caaaacaagtaatggaagcaacatttctatgtgaatagatalsccttgtgtgtgtgt	61800
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QY	6181	gtgcattaaagttgtlaaaggtbaacatgaaacaatggaacttctgtcatataatgtatg	62400
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QY	6361	taagatgataaacaatatactctcttllatctgttctgtcatagtcttcatagaacaactt	64200
Db	6361	TAAATGATAAACAATATATCTCTTTTATGTCTTGTCTATGTTTCATATGAACAATT	64200
QY	6421	cagaatatttltgtlaagtggtgtgcgaatctgaacagctgatttlltttgcattctg	64800
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QY	6481	taagtcacatttgcacatccatttttaactaatatltgcaggttgccttgtatcatgttltg	65400
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QY	6601	agagttcacaccagtttgcgtgttgtagagaaatgaaatgtaaaaaatgctcttcgatg	66600
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QY	6721	aaagcaagaagcagaatcaagaactaagtctcctgtcttcaagttcatgttlltlaagcgct	67800
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QY	6781	tattctgattcaccactgttgcgttgcattcttaatttcaataaactgaaataaagaatg	68400
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QY	6961	gaagagattcccccacacacaaattatattttcttagtaaaagaataacgaattgca	7020
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QY	7021	tcgtggcaatcccttaagcaacatctatctatggaactgcataatcagcaaacacccaga	7080
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QY	7081	agtttgatttaacttggggcaatatgacaagattacattctttgggcaaacactacataag	7140
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QY	7141	caattctctagctgtgcgagacacaaataggcttccttaattttggcagtgatcccttt	7200
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QY	7561	tcttaaatgtgtttttaaagagactattatgtaacgaacttttlaattagaattt	7620
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QY	7681	ccagactaaattgtgtgccattttaaagaactgaataattttaaattttgtctatatt	7740
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QY	7921	caagatatatgaaaaggacagagctctaattgataactctgattccaagaagaaga	7980
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QY	7981	gtaagccaattctctctcacaagaataatggatattttttaaacttaacttaagatag	8040
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MON

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Db 9181 CTCTAGAGCATAGAGTCCCAAAACATCAATCTGTTTCCCGTGTGTTTTTTTTTTTT 9240
QY 9241 tttttcccaatatagaactgagcatalcactttctttctttgtgctgaagttccca 9300
Db 9241 TTTTCCCAATATGAACTGACAGCATACACATCTTTCTTTTGTGCTGAGGTGCTCA 9300
QY 9301 ccgtgaatattgaanaatatatgatatataataatataataataatgtaatgta 9360
Db 9301 CCCTGAATATTGAAAAATATATATATTAATTAATTAATTAATTAATTAATTAATTAATGTA 9360
QY 9361 gtaactgttttgaagaagcattgagatccttggttgaagaagcaccatagagtgccaag 9420
Db 9361 GTACTGTTTGAAGCACTTTAGAGATCCTGTTGGAAGGCAACCATAGAGTGCACAGT 9420
QY 9421 attattatgtggccaaaggggttaatttaactgtaactgtaactgtaactgtaactg 9480
Db 9421 ATTATTAATGTGGCAAGGGGTTATTAACTGTCAGTCCCAAGGCCAAGGAAAGGTTG 9480
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RESULT 2

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 PROGRESS ***, 4 ordered pieces.
 ACCESSION AC013815
 VERSION AC013815.11 GI:18252021
 KEYWORDS HTG; HTGS_PHASE2; HTGS_FULFILL; HTGS_ACTIVEIN.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 165813)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.

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RESULT 4
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DEFINITION Homo sapiens zinc finger protein GC79 mRNA, complete cds.
ACCESSION AF264784
VERSION AF264784.1 GI:10644121
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 5507)
Chang, G.T.G., Steenbeck, M., Schippers, F., Blok, L.J., van
Weerden, M.M., van Alewijk, D.C., Eussen, B.H., van Steenbrugge, G.J.
and Brinkmann, A.O.
Characterization of a Zinc-Finger Protein and Its Association With
Apoptosis in Prostate Cancer Cells
J. Natl. Cancer Inst. 92 (17), 1414-1421 (2000)
10974077
JOURNAL PUBMED
2 (bases 1 to 5507)
AUTHORS Chang, G.T.G.
TITLE Direct Submission
Submitted (09-MAY-2000) Endocrinology & Reproduction, Erasmus
University Rotterdam, P.O.Box 1738, Rotterdam 3000 DR, Netherlands
JOURNAL FEATURES
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RESULT 5
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 DEFINITION Mus musculus atypical GATA protein TRPS1 (trps1) mRNA, complete cds.
 ACCESSION AF346836
 VERSION AF346836.1 GI:13785800
 KEYWORDS house mouse.
 SOURCE Mus musculus.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4452)
 AUTHORS Malik,T.H., Shiochet,S.A., Latham,P., Kroll,T.G., Peters,L.I. and Shivasani,R.A.
 TITLE Transcriptional repression and developmental functions of the atypical vertebrate GATA protein TRPS1
 JOURNAL PUBMED
 EMBO J. 20 (7), 1715-1725 (2001)
 REFERENCE 2 (bases 1 to 4452)
 AUTHORS Malik,T.H. and Shivasani,R.A.
 TITLE Direct Submission
 JOURNAL Submitted (08-FEB-2001) Adult Oncology, Dana Farber Cancer Institute, 44 Binney Street, SM 854, Boston, MA 02115, USA
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GenCore version 4.5
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OK nucleic - nucleic search, using sw model

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(without alignments)

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SUMMARIES

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	2	10255	99.4	10319	21	AAC74759	Breast cancer prot
	3	9951	96.5	10006	22	AAD06861	Human OREX ORE314
C	4	6774.6	65.7	10246	22	ABA14485	Human breast cancer
C	5	6587.2	63.9	10004	22	ABA14483	Human nervous syst
C	6	5793	56.2	5825	22	ABA14484	Human nervous syst
7	2486.4	24.1	2596	22	AAH13738	Human CDNA sequenc	
8	2257.6	21.9	2327	22	AAD06845	Human breast cancer	
9	1580.6	15.3	1587	22	AAH16992	Human CDNA sequenc	

10	1537	14.9	1551	22	AAH15234	Human cDNA sequenc
11	1007	9.8	1009	21	AAC79479	cDNA sequence for
12	943.4	9.1	996	22	AAE44852	Human breast cancer
13	761.4	7.4	766	22	AAE82511	Human breast tumor
14	681.6	6.6	691	22	AAH03167	Human cDNA clone (
15	668.8	6.5	674	22	AAAF44875	Human breast cancer
16	648.6	6.3	813	22	AAH03487	Human cDNA clone (
17	630	6.1	649	22	AAH03278	Human nervous syst
18	621	6.0	664	22	AAH11067	Human breast cancer
19	577.2	5.6	633	22	AAH12431	Human cDNA clone (
20	541.6	5.3	569	22	AAH08818	Human cDNA clone (
21	527.4	5.1	582	22	AAH12558	Human breast cancer
22	520.8	5.0	560	22	AAH08905	Human cDNA clone (
23	474.6	4.6	572	22	AAH09024	Human cDNA clone (
24	453.4	4.4	460	22	AAH21573	Human breast cancer
25	428.4	4.2	451	22	AAH12700	Human breast cancer
26	402	3.9	410	22	AAH20878	Human breast cancer
27	388	3.8	438	22	AAH11991	Human breast cancer
28	384.6	3.7	426	22	AAH23557	Human breast cancer
29	377.4	3.7	415	22	AAH25185	Human breast cancer
30	347.2	3.4	357	22	AAH17790	Human breast cancer
31	345	3.4	357	21	AAC16523	Human breast cancer
32	343	3.3	344	22	AAH10715	Human breast cancer
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34	315.4	3.1	333	19	AAH27248	Human breast cancer
35	315.4	3.1	333	22	AAH43166	Human breast cancer
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ALIGNMENTS

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DT	08-FEB-2001 (first entry)
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KW	antibody; oestrogen receptor; anti-oestrogen; immune response;
KW	lymph node; metastases; tumour; BCR3; BCQ5; BCR1; BCN2;
KW	BCN5; BCQ2; BCN2; BCR3; BCR2; BCR7; BCR3; human; ds.
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PF	15-MAR-2000; 2000WO-US06952.
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PR	12-NOV-1999; 99US-0439878.
PR	12-NOV-1999; 99US-0440370.
PR	15-NOV-1999; 99US-0440493.

FE 22-NOV-2000; 2000MO-US32056.
 PR 23-NOV-1999; 99US-0166973.
 XX (DIAD-) DINDEXUS INC.
 PA Salceda S, Cafferkey R, Recipon H, Sun Y;
 PI WPI; 2001-367602/38.
 DR P-PSDB: AAE02189.
 XX Novel breast cancer specific gene for diagnosing, monitoring, staging,
 PT imaging, preventing and treating cancers, particularly breast cancer
 XX
 PS Claim 1: Page 57-61; 66pp; English.
 CC The invention relates human breast cancer specific genes (BCSG's) and
 CC their corresponding proteins. BCSG is useful for diagnosing, staging,
 CC monitoring, imaging, preventing and treating breast cancers. BCSG is also
 CC useful for inducing an immune response against a target cell expressing
 CC BCSG. The invention also provide methods for detecting genetic lesions or
 CC mutations in BCSG, thereby determining if a human with the genetic lesion
 CC is at risk for breast cancer or has breast cancer. BCSG antibodies
 CC labelled with paramagnetic ions or radioisotopes is useful for imaging
 CC breast cancers, while BCSG antibodies conjugated to a cytotoxic agent is
 CC useful for treating breast cancer. BCSG is useful in the rational design
 CC of new therapeutics for imaging and treating cancers. BCSG is also used
 CC in gene therapy. The present DNA sequence is human breast cancer specific
 CC gene-3 (BCSG-3) or Gene ID 274731.
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